

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 1, 2004, 12:07:39 ; Search time 80.3158 Seconds
(without alignments)
1561.731 Million cell updates/sec

Title: US-09-095-478A-7_COPY_188_405

Perfect score: 1174

Sequence: 1 QNRDKNRYRDILPYDSTRVP.....DIMNIVTQMRKQRCGMIOQK 218

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1174	100.0	426	2 O55082	O55082 mus musculus
2	928	79.0	398	2 Q9Y406	Q9Y406 homo sapien
3	556.5	47.4	2484	2 Q28006	Q28006 bos taurus
4	550.5	46.9	2453	1 PTND MOUSE	Q64512 mus musculus
5	541.5	46.1	2485	1 PTND HUMAN	Q12923 homo sapien
6	541.5	46.1	2500	2 Q6BHH9	Q6BHH9 xenopus lae
7	479	40.8	920	2 Q6GPK7	Q6GPK7 xenopus lae
8	468	39.9	252	2 Q8N4S3	Q8N4S3 homo sapien
9	467	39.8	913	1 PTN3 HUMAN	P26045 homo sapien
10	461.5	39.3	926	2 Q9WU22	Q9WU22 mus musculus
11	453.5	38.6	1222	2 Q8MY44	Q8MY44 eptaretus
12	452.5	38.5	1100	2 Q8MY45	Q8MY45 eptaretus
13	452.5	38.5	1187	2 Q8MY42	Q8MY42 eptaretus
14	452.5	38.5	1202	2 Q8MY43	Q8MY43 eptaretus
15	449.5	38.3	1998	2 Q8CIW2	Q8CIW2 mus musculus
16	448.5	38.2	907	2 Q8MY41	Q8MY41 eptaretus
17	447.5	38.1	1102	2 Q8OVN7	Q8OVN7 mus musculus
18	446.5	38.0	579	2 Q9J307	Q9J307 mus musculus
19	445.5	37.9	1956	2 Q6MZF6	Q6MZF6 homo sapien
20	445.5	37.9	1956	2 CAE46198	CAE46198 homo sapi
21	445.5	37.9	1997	1 PTNB HUMAN	P23467 homo sapien
22	444.5	37.9	926	1 PTN4 HUMAN	P29074 homo sapien
23	444	37.8	1337	1 PTPJ HUMAN	Q12913 homo sapien
24	441.5	37.6	929	2 Q6NRE9	Q6NRE9 xenopus lae
25	441.5	37.6	929	2 Q6DCH9	Q6DCH9 xenopus lae
26	441.5	37.6	929	2 AAH70687	AAH70687 xenopus l
27	439	37.4	1238	2 Q8K3Q2	Q8K3Q2 mus musculus
28	438.5	37.4	1216	2 Q9IBD8	Q9IBD8 cyprinus ca
29	437.5	37.3	1948	1 PTNS HUMAN	Q13332 homo sapien
30	437.5	37.3	2051	2 Q4328	Q4328 hirudo medi
31	437	37.2	1216	2 Q62884	Q62884 rattus norv

32	436	37.1	361	2	Q61373	Q61373 mus musculus
33	436	37.1	382	1	PTN2 MOUSE	Q06180 mus musculus
34	436	37.1	406	2	Q922E7	Q922E7 mus musculus
35	436	37.1	1238	1	PTPJ MOUSE	Q64455 mus musculus
36	436	37.1	1238	2	AAK96030	AAK96030 mus muscu
37	434.5	37.0	468	2	Q9IBA0	Q9IBA0 potamotrygo
38	434.5	37.0	615	2	Q9IAI8	Q9IAI8 xenopus lae
39	434	37.0	353	2	Q96AUS	Q96AUS homo sapien
40	434	37.0	363	1	PTN2 RAT	P35233 rattus norv
41	434	37.0	415	1	PTN2 HUMAN	P17706 homo sapien
42	434	37.0	1457	1	PTPK MOUSE	P35822 mus musculus
43	432.5	36.8	468	2	Q9IBA2	Q9IBA2 potamotrygo
44	432.5	36.8	1502	2	Q9UM81	Q9UM81 homo sapien
45	432.5	36.8	1912	1	PTPD_HUMAN	P23468 homo sapien

ALIGNMENTS

RESULT 1

O55082	AC	O55082	PRELIMINARY;	PRT;	426 AA.
DT	01-JUN-1998	(TREMBLrel. 06, Created)			
DT	01-JUN-1998	(TREMBLrel. 06, Last sequence update)			
DT	01-OCT-2004	(TREMBLrel. 28, Last annotation update)			
DE	Protein-tyrosine-phosphatase (EC 3.1.3.48) (Mus musculus adult male				
DE	testis cDNA, RIKEN full-length enriched library, clone:4921505B14				
DE	product:protein tyrosine phosphatase, non-receptor type 20, full				
DE	insert sequence).				
GN	Name=Ptpn20;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Testis;				
RX	MEDLINE=98070510; PubMed=9407093;				
RA	Ohsugi M., Kuramochi S., Matsuda S., Yamamoto T.;				
RT	"Molecular cloning and characterization of a novel cytoplasmic				
RT	protein-tyrosine phosphatase that is specifically expressed in				
RT	spermatocytes.";				
RL	J. Biol. Chem. 272:33092-33099(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Testis;				
RX	MEDLINE=99279253; PubMed=10349636;				
RA	Carninci P., Hayashizaki Y.;				
RT	"High-efficiency full-length cDNA cloning.";				
RL	Meth. Enzymol. 303:19-44(1999).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Testis;				
RX	MEDLINE=21085660; PubMed=11217851;				
RA	RIKEN FANTOM Consortium;				
RT	"Functional annotation of a full-length mouse cDNA collection.";				
RL	Nature 409:685-690(2001).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Testis;				
RA	The FANTOM Consortium,				
RT	the RIKEN Genome Exploration Research Group Phase I & II Team;				
RT	"Analysis of the mouse transcriptome based on functional annotation of				
RT	60,770 full-length cDNAs.";				
RL	Nature 420:563-573(2002).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Testis;				
RX	MEDLINE=20499374; PubMed=11042159;				
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,				
RA	Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;				
RT	"Normalization and subtraction of cap-trapper-selected cDNAs to				

RT prepare full-length cDNA libraries for rapid discovery of new genes.;"
RL Genome Res. 10:1617-1630(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakauchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RC "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.;"
RL Genome Res. 10:1757-1771(2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; D64141; BAA23761.1; -.
DR EMBL; AK029493; BAC26476.1; -.
DR HSP; P10586; ILAR.
DR MGD; MGI:1196295; Ptpn20.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; Tyr_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; Ptpc; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase; Receptor.
FT Non TER 1
SQ SEQUENCE 426 AA; 49118 MW; 2B35FB13379502F4 CRC64;

Query Match 100.0%; Score 1174; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.8e-106;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNRDKNRYDILPYDSTRVPLGKKNKYINASYIRIVNHEEYFYIATQGLPETIEDFWQ 60
DB 188 QNRDKNRYDILPYDSTRVPLGKKNKYINASYIRIVNHEEYFYIATQGLPETIEDFWQ 247

QY 61 MVLNNCNVIAITREIECGVICKYSYWPISLKEPLPEHFSVLETFHVTQYFTVRVQ 120
DB 248 MVLNNCNVIAITREIECGVICKYSYWPISLKEPLPEHFSVLETFHVTQYFTVRVQ 307

QY 121 IVKSTGKSCQVKHLQFTKWDHGTTPASADFFIKYRVYVRKSHITGPIIVHCSAGVGTG 180
DB 308 IVKSTGKSCQVKHLQFTKWDHGTTPASADFFIKYRVYVRKSHITGPIIVHCSAGVGTG 367

QY 181 VFICVDVVFSALIEKNYSFDIMNIVTQMRKQRCGMIOTK 218
DB 368 VFICVDVVFSALIEKNYSFDIMNIVTQMRKQRCGMIOTK 405

RESULT 2
QY406

ID QY406 PRELIMINARY; PRT; 398 AA.
AC QY406;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein DKFZp566K0524 (Fragment).
GN Names=DKFZp566K0524;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Ansoorge W., Wirkner U., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050040; CAB43248.1; -.
DR PIR; T08716; T08716.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; Tyr_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; Ptpc; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase; Hypothetical protein.
FT Non TER 1
SQ SEQUENCE 398 AA; 45690 MW; 857AAD03747870A2 CRC64;

Query Match 79.0%; Score 928; DB 2; Length 398;
Best Local Similarity 77.9%; Pred. No. 2.2e-82;
Matches 169; Conservative 24; Mismatches 24; Indels 0; Gaps 0;

QY 2 NRDKNRYDILPYDSTRVPLGKKNKYINASYIRIVNHEEYFYIATQGLPETIEDFWQM 61
DB 161 NRDKNRYDILPYDSTRVPLGKKNKYINASYIRIVNHEEYFYIATQGLPETIEDFWQM 220

QY 62 VLENNCNVIAITREIECGVICKYSYWPISLKEPLPEHFSVLETFHVTQYFTVRVQI 121
DB 221 VLENNCNVIAITREIECGVICKYSYWPISLKEPLPEHFSVLETFHVTQYFTVRVQI 280

QY 122 VKSTGKSCQVKHLQFTKWDHGTTPASADFFIKYRVYVRKSHITGPIIVHCSAGVGTG 181
DB 281 VKSTGKSCQVKHLQFTKWDHGTTPASADFFIKYRVYVRKSHITGPIIVHCSAGVGTG 340

QY 182 FICVDVVFSALIEKNYSFDIMNIVTQMRKQRCGMIOTK 218
DB 341 FICVDVVFSALIEKNYSFDIMNIVTQMRKQRCGMIOTK 377

RESULT 3
Q28006 PRELIMINARY; PRT; 2484 AA.
ID Q28006
AC Q28006;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE BA14.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Vega O.C., Walton K.M., Dixon J.F.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 5 PDZ/DHR domains.
DR EMBL; U20807; AAA73516.1; -.

```
DR HSP; Q64512; LGM1.
DR GO:0005856; C:cytoskeleton; IEA.
DR GO:0016787; F:hydrolase activity; IEA.
DR GO:0005515; F:protein binding; IEA.
DR GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro: IPR000299; Band.4.1.
DR InterPro: IPR009065; FERM.
DR InterPro: IPR011009; Kinase_like.
DR InterPro: IPR011019; KIND.
DR InterPro: IPR001478; PDZ.
DR InterPro: IPR011036; PH_related.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PF00373; Band.41; 1.
DR Pfam: PF00595; PDZ; 5.
DR Pfam: PF00102; Y_phosphatase; 1.
DR PRINTS: PR00935; BAND41.
DR PRINTS: PR00700; PRTPHPTASE.
DR SMART: SM00295; B41; 1.
DR SMART: SM00750; KIND; 1.
DR SMART: SM00228; PDZ; 5.
DR SMART: SM00194; PTEC; 1.
DR PROSITE: PS00660; FERM_1; FALSE_NEG.
DR PROSITE: PS00661; FERM_2; FALSE_NEG.
DR PROSITE: PS00577; FERM_3; 1.
DR PROSITE: PS01066; PDZ; 5.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
SQ SEQUENCE 2484 AA; 276382 MW; 45A92F0D4F1ED13D CRC64;

Query Match 47.4%; Score 556.5; DB 2; Length 2484;
Best Local Similarity 48.4%; Pred. No. 5.7e-45;
Matches 106; Conservative 36; Mismatches 76; Indels 1; Gaps 1;

QY 1 QNRDNKRYDILPYSTRVPLGKNDYINASIRVNHHEEYFYATQPLPETHDFWQ 60
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2235 ENRKNRYKNILPYDATVPLGDEGKYNASFIKIPVGEEFYIACQGLPETHDFWQ 2294

QY 61 MVLNNCNVIMTRIECGVICKISYWPISL-KEPLEFEHSVLETHVTOYFTVRF 119
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2295 MIWEQSSVIMMTQEVGEKIKQRYWPNVLGKSTMVSNRLRLVVRVQQLKGFVVRAM 2354

QY 120 QIVKSTGKSCQVKHLQFTKWPDPHGTPASADFFIKYRVYRKSHITGPLLHCSAGVGR 179
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2355 TLEDIQTGEVRVSHLNFATWPDHDTSPQDDLLTFISYMRHVHRSPIITHCSAGIGRS 2414

QY 180 GVFCVDDVFSAEKKNYSFDIMNVITQMRKQRCMIQTK 218
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:
2415 GTLICIDVVLGLISQDLEFIDSLVRCMLQRHGMVQTE 2453

RESULT 4
PTND MOUSE STANDARD; PRT; 2453 AA.
AC Q64512; Q61494; Q62135; Q64499;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 13 (EC 3.1.3.48)
DE (Protein tyrosine phosphatase PTP-BL) (protein-tyrosine phosphatase
DE RIP) (protein tyrosine phosphatase PTP) (PTP36).
GN Name=Ptpn13; Synonyms=Ptp14;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN _
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6; TISSUE=Skin;
RX MEDLINE=96340953; PubMed=8749712;
```

PDB; 1021; NMR; A=1351-1444.
DR MGD; MGI:103293; Ptpn13.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR009065; FERM.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00373; Band 4.1.
DR Pfam; PF00595; PDZ_5.
DR PRINTS; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00935; BAND4.1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00295; B41; 1.
DR SMART; SM00228; PDZ; 5.
DR SMART; SM00194; PTPC; 1.
DR SMART; SM00404; PTPC motif; 1.
DR PROSITE; PS00660; FERM 1; FALSE NEG.
DR PROSITE; PS00661; FERM 2; FALSE NEG.
DR PROSITE; PS50057; FERM 3; 1.
DR PROSITE; PS50106; PDZ_5.
DR PROSITE; PS00383; TYR PHOSPHATASE 1; FALSE NEG.
DR PROSITE; PS50056; TYR PHOSPHATASE 2; 1.
DR PROSITE; PS50055; TYR PHOSPHATASE FTP; 1.
DR 3D-structure; Coiled coil; Cytoskeleton; Hydrolase;
KW Protein phosphatase; Repeat; Structural protein.
FT DOMAIN 458 493 Coiled coil (Potential).
FT DOMAIN 565 865 FERM.
FT DOMAIN 1084 1170 PDZ 1.
FT DOMAIN 1357 1442 PDZ 2.
FT DOMAIN 1491 1579 PDZ 3.
FT DOMAIN 1764 1845 PDZ 4.
FT DOMAIN 1857 1942 PDZ 5.
FT DOMAIN 2180 2434 Protein-tyrosine phosphatase.
FT ACT_SITE 2375 2375 Phosphocysteine intermediate (By similarity).
FT DOMAIN 56 59 Poly-Leu.
FT CONFLICT 79 81 STA -> FTG (in Ref. 2).
FT FT HIRNSNCAPFSN -> TSGTASRAFTVSY (in Ref. 2).
FT FT V -> L (in Ref. 2).
FT CONFLICT 233 233 N -> I (in Ref. 2).
FT CONFLICT 306 306 K -> E (in Ref. 2).
FT CONFLICT 322 322 Q -> K (in Ref. 2).
FT CONFLICT 381 381 S -> L (in Ref. 2).
FT CONFLICT 822 822 S -> T (in Ref. 3).
FT CONFLICT 1233 1233 R -> Q (in Ref. 2).
FT CONFLICT 1449 1449 QTPHVKDYSFVTEEDNT -> KHPMSKTTALLKII (in Ref. 1).
FT CONFLICT 1474 1489 Ref. 1).
FT CONFLICT 1622 1622 D -> H (in Ref. 2).
FT CONFLICT 1872 1872 S -> P (in Ref. 1).
FT CONFLICT 1979 1979 N -> I (in Ref. 3).
FT CONFLICT 2078 2078 D -> N (in Ref. 2).
FT CONFLICT 2233 2233 S -> T (in Ref. 2).
FT CONFLICT 2448 2452 PGLPQ -> GSHSDAQPKAPP (in Ref. 1).
SQ SEQUENCE 2453 AA; 270332 MW; 53396F27AE2582F2 CRC64;
Query Match 46.9%; Score 550.5; DB 1; Length 2453;
Best Local Similarity 49.5%; Pred. No. 2.2e-44;
Matches 110; Conservative 34; Mismatches 71; Indels 7; Gaps 3;
QY 1 QNRDNRYRDLFDYSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
DB 2203 ENRRKNRYKNILFYDTRFVLGDEGGYINASFIRIPVGTQEFYIACQGPLPTTGDFWQ 2262
QY 61 MYLENNCNVIAMTRIEICGVKICYSWPISL-KEPLEFEHFSVFLTEHVTQYFVRVF 119
DB 2263 MYWEQNSQTVIAMTWQVEGEKIKCQYFWSILGTTMANERLRLALLRQQLKGFTVRYM 2322
QY 120 QIVKKSQKSCQVKHLQFTKWPDPHGTGPAGD---PFIKYRVYVRKSHITGPLLVHCSAGV 176
DB 2323 ALEDQTGTGEVRHLSHLNFTAWPDHPTPSQDDLLTIFISWRIHRS---GPVITHCSAGI 2379
QY 177 GRIGVFICVDVVFSAIEKNYSFDMINVTQMRKQRCGMIOTK 218

DB 2380 GRSGLTICIDVVLGLISQDLFEFDISLVRCMLQRHGMVQTE 2421
RESULT 5
PTND HUMAN STANDARD; PRT: 2485 AA.
AC Q12923; Q15159; Q15263; Q15264; Q15265; Q15674; Q16826; Q81WH7;
AC Q9NYN9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 13 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase 1E) (PTP-EL) (hPTPE1) (PTP-BAS)
DE (Protein-tyrosine phosphatase FPL1) (fas-associated protein-tyrosine phosphatase 1) (FAP-1).
DE Phosphatase 1 (FAP-1).
GN Name=PTPN13; Synonyms=PTP1E, PTP1L, PNP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORM 4).
RP TISSUE=Breast carcinoma;
RX MEDLINE=94350988; PubMed=8071359;
RA Banville D., Ahmad S., Stocco R., Shen S.-H.;
RT "A novel protein-tyrosine phosphatase with homology to both the cytoskeletal proteins of the band 4.1 family and junction-associated guanylate kinases.";
RL J. Biol. Chem. 269:22320-22327(1994).
RN [2]
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RP TISSUE=Leukemia;
RX MEDLINE=94116679; PubMed=8287977;
RA Maekawa K., Imagawa N., Nagamatsu M., Harada S.;
RT "Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane-binding domain and GLGF repeats.";
RL FEBS Lett. 337:200-206(1994).
RN [3]
SEQUENCE FROM N.A.
RP TISSUE=Fibroblast;
RX MEDLINE=95014139; PubMed=7929060;
RA Saras J., Claesson-Welsh L., Heldin C.-H., Gonen L.J.;
RT "Cloning and characterization of pPPL1, a protein tyrosine phosphatase with similarities to cytoskeletal-associated proteins.";
RL J. Biol. Chem. 269:24082-24089(1994).
RN [4]
SEQUENCE OF 1216-2490 FROM N.A.
RP TISSUE=Pancreas;
RA Wang H.Y.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
RN [5]
SEQUENCE OF 1279-1883 FROM N.A. (ISOFORM 4).
RP TISSUE=Brain;
RX MEDLINE=95232528; PubMed=7536343;
RA Sato T., Irie S., Kitada S., Reed J.C.;
RT "FAP-1: a protein tyrosine phosphatase that associates with Fas.";
RL Science 268:411-415(1995).
RN [6]
SEQUENCE OF 1323-1821 FROM N.A.
RA Irie S., Hachiya T., Sato T.A.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
SEQUENCE OF 1323-1922 FROM N.A.
RP TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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Query Match      46.1%; Score 541.5; DB 1; Length 2485;
Best Local Similarity 47.0%; Pred. No. 1.7e-43;
Matches 103; Conservative 37; Mismatches 78; Indels 1; Gaps 1;

Qy 1 QNRDKNRYRDIILPYDSTRVPLGKNKDYINASYIRIVNHEREEYPIATQGLPEITDFWQ 60
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 2236 ENRRKRYKNILPYDATRPVLGDEGGYINASFIPVKGEFFYVIAQCGELPTTVGDFWQ 2295
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy 61 MVLNNCNVIAMTTRTEICGVIIKCYSWPISL-KEPLEFEHFHSVFLTFTHVYQYFTRVRF 119
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 2296 MIWEQKSTVIAMMTQVEGEKIKQRYPWNLGKTTMVSNRRLRALVRMQLKGFVVRAM 2355
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

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Qy	120	QIVKSGKSGQCVKQKHLOFTKWDHGTSPASADFFIKYVYVRKSHITGPIILVHCSAGVGT	179
Db	2356	TLEDIQREVRHSHLNTAPWDHDTSPQDDLLTFSYMRHHRSGPIITHCSAGIGRS	2415
Qy	180	GVFFCVDDVFSAEKNYSFDIMNIVTQMRKQRCGMIQTK	218
Db	2416	GTUICIDVWGLISQSDLDFDISIVRCWRIQRHGVMQTE	2454

RESULT 6

ID	QSEHH9	PRELIMINARY;	PRT; 2500 AA.
AC	QSEHH9;		
DT	01-OCT-2004	(TREMBlrel. 28, Created)	
DT	01-OCT-2004	(TREMBlrel. 28, last sequence update)	
DT	01-OCT-2004	(TREMBlrel. 28, last annotation update)	
DE	Prizzled-8 associated multidomain protein (Fragment).		
DE	Name=FRTD;		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Lisovsky M.Y., Itch K., Sokol S.Y.;		
RL	Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY327257; AAR97566.1; -.		
DR	NON TER 2500		
FT	SEQUENCE 2500 AA; 277694 MW; D0DD27366EA19CA0 CRC64;		

RESULT 7

ID	Q6GPK7	PRELIMINARY;	PET;	920 AA.
AC	Q6GPK7;			
DT	05-JUL-2004	(TREMBLrel. 27, Created)		
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)		
DE	Hypothetical protein.			
OS	Xenopus laevis	(African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Oocytes;			
RC	MEDLINE=22389257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			

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Db 790 YVFRMLTDTTGTGDEFPPIIHLOYVAMPDHGVPDDSSDFLEFATVVRQKRMENQVPLVHC 849
QY 173 SAGVGRGTGVFCVDDVVSFAIEKNYSFDMNIVTQMRKQRCGMQIOT 217
Db 850 SAGVGRGTGVLTMTMETAMCLIEHQVYPVLDVVQRMDQRAMVQIOT 894

RESULT 8
Q8N4S3 PRELIMINARY; PRT; 292 AA.
AC Q8N4S3;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033716; AAH33716.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_FTP; 1.
KW Hydrolase; Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 292 AA; 33121 MW; 54B838BDD41D1BD7 CRC64;

Query Match 39.9%; Score 468; DB 2; Length 292;
Best Local Similarity 42.3%; Pred. No. 2e-37;
Matches 96; Conservative 35; Mismatches 78; Indels 18; Gaps 5;

QY 1 QNRDKNRYDILPVDSTRVPLGKNDYINASYI-----RIVNHEEYFYIAQTQGLPE 53
Db 48 QNLDKNRYKDVLYDTITRVLLQGNEDYINASYVNMETPAANLVNK-----YIATQGLPLH 102
QY 54 TIEDFWQMLNENCNVAMITREIECGVIKCYSWPISLKEPLEFEH--FSVFELETFHVT 111
Db 103 TCAQFWQVWVDQKLSLIVMLTTLTTERGTRKCHQWYP---DPPDVNMHGGFHIQCQSDCT 159
QY 112 QYFTVRVQVVKKSGKQCXKHLQFTKPDHGPASADFFIKKRVYVRKSHI--TGPLLV 170
Db 160 IAVSRMLVNTQGTGEHTVHTLQYVWPDHGVDPDSSDFLEFVNVRSIRVDSSEPLV 219
QY 171 HCSAGVGRGTGVFCVDDVVSFAIEKNYSFDMNIVTQMRKQRCGMQIOT 217
Db 220 HCSAGIGRTGVLTMTMETAMCLITERNLPYPLDVRKMDQRAMVQIOT 266

RESULT 9
PTN3 HUMAN
ID PTN3 HUMAN STANDARD; PRT; 913 AA.
AC P26045;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 3 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase H1) (PTP-H1).
GN Name=PTPN3; Synonyms=PTPH1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Yang Q., Tonks N.K.;
RT "Isolation of a cDNA clone encoding a human protein-tyrosine
RT phosphatase with homology to the cytoskeletal-associated proteins band
RT 4.1, ezrin, and talin.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5949-5953(1991).
RN [2]
RP SEQUENCE OF 194-896 FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=93227504; PubMed=1626183;
RA Arimura Y., Hinoda Y., Itoh F., Takekawa M., Tsujisaki M., Adachi M.,
RA Imai K., Yachi A.;
RT "cDNA cloning of new protein tyrosine phosphatases in the human
RT colon.";
RL Tumour Biol. 13:180-186(1992).
RN [3]
RP SEQUENCE OF 899-913 FROM N.A.
RX MEDLINE=95179278; PubMed=7874267;
RA Ikuta S., Itoh F., Hinoda Y., Toyota M., Makiguchi Y., Imai K.,
RA Yachi A.;
RT "Expression of cytoskeletal-associated protein tyrosine phosphatase
RT PTPH1 mRNA in human hepatocellular carcinoma.";
RL J. Gastroenterol. 29:727-732(1994).
CC -!- FUNCTION: May act at junctions between the membrane and the
CC cytoskeleton.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -!- SIMILARITY: Contains 1 FERM domain.
CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
EMBL; M64572; AAA35647.1; -.
DR EMBL; S39392; AAB22439.2; -.
DR EMBL; S76309; AAB33583.1; -.
DR PIR; A41109; A41109.
DR HSSP; P18031; 1C88.
DR Genew; HGNC:9655; PTPN3.
DR MIM; 176877; -.
DR GO; GO:0004725; F:protein-tyrosine-phosphatase activity; TAS.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR000798; Bz/rad/moesin.
DR InterPro; IPR009065; FERM.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR011036; PH-related.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00373; Band_41; 1.
DR Pfam; PF00595; PDZ; 1.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00935; BAND41.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00295; B41; 1.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00660; FERM_1; 1.
DR PROSITE; PS00661; FERM_2; 1.
DR PROSITE; PS50057; FERM_3; 1.
DR PROSITE; PS50106; PDZ; 1.
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DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_FTP; 1.
KW Cytoskeleton; Hydrolase; Protein phosphatase; Structural protein.
FT DOMAIN 29 312 FERM.
FT FT 510 582 PDZ.
FT DOMAIN 670 913 Protein-tyrosine phosphatase.
FT ACT_SITE 842 842 Phosphotyrosine intermediate (By
similarity).
SQ SEQUENCE 913 AA; 104029 MW; 29A539ACDE2F1515 CRC64;
Query Match 39.8%; Score 467; DB 1; Length 913;
Best Local Similarity 42.3%; Pred. No. 1e-36;
Matches 96; Conservative 35; Mismatches 78; Indels 18; Gaps 5;
QY 1 QNRDKRYRDLIPYDSTRVPLGKNKYINASYI-----RIVNHEEYFYIATQGLPE 53
DB 669 QNRDKRYRDLIPYDSTRVPLGKNKYINASYI-----RIVNHEEYFYIATQGLPH 723
QY 54 TIEDFWQWMLNENCNVIAITREICGVKICYSWPIISLKEPLEFEH--FSVFLTEPHVT 111
DB 724 TCAQFQVQVWDQKLSLIVMLTITERTGRTKCHQWP---DPPDVNHEGGFHIQCQSDCT 780
QY 112 QYTVTRVFOIVKXSTGKSCQKHLQFTKPDHGTGPASADFFIKYVYVRKSHI--TEPLLV 170
DB 781 IAYVSRMLVTNTQTGEHTVTHLQYVAVPDHGIPTDSSDFLEFVNVYVRSRLVDSBPVLV 840
QY 171 HCSAGVGRGTGVFCVDVWFSAIEKYSFDMNIVTQMKRCQGMQIQT 217
DB 841 HCSAGIGRTGVLTMTAMCLTERNLPIYPLDIVRKMRDQAMVQIQT 887
RESULT 10
Q9WU22 PRELIMINARY; PRT; 926 AA.
ID Q9WU22
AC Q9WU22
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Testis-enriched protein tyrosine phosphatase.
GN Name=Ptpn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=20510023; PubMed=11054567;
RA Park K.W., Lee E.J., Lee S.H., Lee J.E., Choi E.Y., Kim B.J.,
RA Hwang R., Park K.A., Baik J.H.;
RT "Molecular cloning and characterization of a protein tyrosine
RT phosphatase enriched in testis, a putative murine homologue of human
RT PTPMBG";
RL Gene 257:45-55(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Choi E.-Y., Park K.-W., Lee E.-J., Baik J.-H.;
RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Contains 1 PDZ/DHR domain.
DR EMBL; AF106702; AAD22773.1; -.
DR HSSP; P11171; 1GG3.
DR MGD; MGI:1099792; Ptpn4.
DR GO; GO:0004726; F.non-membrane spanning protein tyrosine phos. . . ; IDA.
DR InterPro; IPR000299; Band_4.1.
DR InterPro; IPR000798; Ez/rad/moesin.
DR InterPro; IPR000965; FERM.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR011036; PH related.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
FRam; PF00373; Band_41; 1.

DR Pfam; PF00595; PDZ; 1.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00935; BAND41.
DR PRINTS; PR00661; ERMFAMILY.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00295; B41; 1.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00660; FERM_1; UNKNOWN_1.
DR PROSITE; PS00661; FERM_2; 1.
DR PROSITE; PS00057; FERM_3; 1.
DR PROSITE; PS0106; PDZ; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_FTP; 1.
KW Hydrolase.
SQ SEQUENCE 926 AA; 105713 MW; A344DAD4FF7E2AE2 CRC64;
Query Match 39.3%; Score 461.5; DB 2; Length 926;
Best Local Similarity 41.5%; Pred. No. 3.6e-36;
Matches 95; Conservative 39; Mismatches 74; Indels 21; Gaps 5;
QY 1 QNRDKRYRDLIPYDSTRVPLGKNKYINASYI-----RIVNHEEYFYIATQGLPE 53
DB 678 QNRDKRYRDLIPYDSTRVPLGKNKYINASYI-----RIVNHEEYFYIATQGLPH 732
QY 54 TIEDFWQWMLNENCNVIAITREICGVKICYSWPIISLKEPLEFEHFSVFLTEPHVTQ- 112
DB 733 TCKDFQWMIWEQSSMVVMLTTQVERGRVKCHQWP---EPSESSSYGCYQATCHSEEG 788
QY 113 --YFTVTRVFOIVKXSTGKSCQKHLQFTKPDHGTGPASADFFIKYVYVR--KSHITGPL 168
DB 789 NPAYIFRKMVLINQEKNSRQLTQIQTAMPDGHGVDDSDFLDFVCHVRDQAGKEEPI 848
QY 169 LVHCSAGVGRGTGVFCVDVWFSAIEKYSFDMNIVTQMKRCQGMQIQT 217
DB 849 LVHCSAGIGRTGVLTMTAMCLTERNLPIYPLDIVRKMRDQAMVQIQT 897
RESULT 11
Q8MY44 PRELIMINARY; PRT; 1222 AA.
ID Q8MY44
AC Q8MY44;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CD45 (Fragment).
GN Name=PTPRC;
OS Eptaretus stoutii (Pacific hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
OC Myxiniidae; Eptaretinae; Eptaretus.
OX NCBI_TaxID=7765;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22131575; PubMed=12136341;
RA Nagata T., Suzuki T., Ohta Y., Flajnik M.P., Kasahara M.;
RT "The leukocyte common antigen (CD45) of the Pacific hagfish,
RT Eptaretus stoutii: implications for the primordial function of
RT CD45";
RL Immunogenetics 54:286-291(2002).
DR EMBL; AB078866; BAC06501.1; -.
DR GO; GO:0016787; F.hydrolase activity; IEA.
DR GO; GO:0004725; F.protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P.protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00194; PTPC; 2.

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DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase. 1222 1222
FT NON_TER 1222 1222
SQ SEQUENCE 1222 AA; 137895 MW; 1A3965AA3E6B4B69 CRC64;

Query Match
Best Local Similarity 42.9%; Pred. No. 3.4e-35; Length 1222;
Matches 96; Conservative 28; Mismatches 89; Indels 11; Gaps 4;

QY 2 NRDKNRYRDLIPYDSTRVPLGKN-----KDYINASYIRIVNHEEYFYIATOGPLPETIE 56
Db 620 NNGKNRYSDILPYDNNRVLVNSGGKPGSDYINASYIN--GYKESKKYICAQGPMEETA 677
QY 57 DFWQVLENNCNVIAITREIECGVIKCYSWPISLKEPLEFHFVSFLETFHTVQYFTV 116
Db 678 EFWTMIWEQKTAIVIMVTRCIEGGKKNKYQYWPQKGLKLEFKLSV--TNEVMLYPDY 735
QY 117 RVFQIVKKGSTGKSCQVKHLQFTKWDHGTTPASADFFIKYRVYRK--SHITGPLLHCSA 174
Db 736 IITEISLHGGNSRIITHVQFTKWDHGVDPDPLLRLRRRLVLSFCNFFDGMVHVCSA 795
QY 175 GVGRTGVFCVDVFAIEKNYSFDMNIVTOMRKORCGMIQTK 218
Db 796 GVGRSGTFAISLMEMLDEGRIDVYGFVSLRQORCLMVQVE 839

RESULT 12
Q8MY45 PRELIMINARY; PRT; 1100 AA.
AC Q8MY45;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE CD45 (Fragment);
GN Name=PTPRC;
OS Eptatretus stoutii (Pacific hagfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
OC Myxiniidae; Eptatretinae; Eptatretus.
OX NCBI_TaxID=7765;
RN [1]
RX MEDLINE=22131575; PubMed=12136341;
RA Nagata T., Suzuki T., Ohta Y., Flajnik M.F., Kasahara M.;
RT "The leukocyte common antigen (CD45) of the Pacific hagfish,
RT Eptatretus stoutii: implications for the primordial function of
RT CD45.";
RL Immunogenetics 54:286-291(2002).
DR EMBL; AB078865; BAC06500.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase.
FT NON_TER 1 1
FT NON_TER 1100 1100
SQ SEQUENCE 1100 AA; 2159D62FDBD919BB CRC64;

Query Match
Best Local Similarity 38.5%; Score 452.5; DB 2; Length 1100;
Matches 96; Conservative 28; Mismatches 89; Indels 11; Gaps 4;

QY 2 NRDKNRYRDLIPYDSTRVPLGKN-----KDYINASYIRIVNHEEYFYIATOGPLPETIE 56
Db 585 NNGKNRYSDILPYDNNRVLVNSGGKPGSDYINASYIN--GYKESKKYICAQGPMEETA 642
QY 57 DFWQVLENNCNVIAITREIECGVIKCYSWPISLKEPLEFHFVSFLETFHTVQYFTV 116
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OM protein - protein search, using sw model

Run on: December 1, 2004, 12:07:42 ; Search time 18.4854 Seconds
(without alignments)
1134.694 Million cell updates/sec

Title: US-09-095-478A-7_COPY_188_405

Perfect score: 1174

Sequence: 1 QNRDKNRYRDLPYDSTRVP.....DIMNIVTQMKQRCGMIOYK 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79: *
1: piri: *
2: piri: *
3: piri: *
4: piri: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	928	79.0	398	2 T08716	protein-tyrosine-p
2	547.5	46.6	2450	2 S71625	protein-tyrosine-p
3	541.5	46.1	2294	2 I67630	protein-tyrosine-p
4	541.5	46.1	2466	2 I67629	protein-tyrosine-p
5	533.5	45.4	2490	1 A54971	protein-tyrosine-p
6	467	39.8	913	1 A41109	protein-tyrosine-p
7	448.5	38.2	583	2 S17671	protein-tyrosine-p
8	445.5	37.9	1997	1 S12050	protein-tyrosine-p
9	444.5	37.9	926	1 A41105	protein-tyrosine-p
10	444	37.8	1337	1 I38670	protein-tyrosine-p
11	437.5	37.3	2051	2 T30938	protein-tyrosine-p
12	436	37.1	382	1 A38191	receptor tyrosine
13	436	37.1	1238	2 S68700	HPTP beta-like tyr
14	435	37.1	387	1 A60345	protein-tyrosine-p
15	434	37.0	363	1 S14294	protein-tyrosine-p
16	434	37.0	415	1 A33899	protein-tyrosine-p
17	434	37.0	1457	1 A48066	protein-tyrosine-p
18	432.5	36.8	1912	2 A56178	protein-tyrosine-p
19	431	36.7	1198	1 A57064	protein-tyrosine-p
20	431	36.7	1216	2 S60613	protein-tyrosine-p
21	430	36.6	405	2 I59372	protein-tyrosine-p
22	427.5	36.4	1176	2 I58345	protein-tyrosine-p
23	427.5	36.4	1501	2 I58148	protein-tyrosine-p
24	427.5	36.4	1907	2 S05893	protein-tyrosine-p
25	427	36.4	405	2 S68250	protein-tyrosine-p
26	427	36.4	1187	1 A53661	protein-tyrosine-p
27	425.5	36.2	1262	1 A48758	protein-tyrosine-p
28	425.5	36.2	1496	1 A48758	protein-tyrosine-p
29	425.5	36.2	1863	2 S46217	protein-tyrosine-p

30 425 36.2 356 2 JW0049 protein-tyrosine-p
31 424 36.1 1187 1 JC4155 protein-tyrosine-p
32 424 36.1 1273 1 TDRILT leukocyte common a
33 423 36.0 1226 2 JC7503 protein-tyrosine-p
34 423 36.0 1452 1 S17669 protein-tyrosine-p
35 422.5 36.0 1174 2 I38140 protein-tyrosine-p
36 422 35.9 1452 1 S17670 protein-tyrosine-p
37 421 35.9 597 2 B53978 protein-tyrosine-p
38 421 35.9 694 2 A53978 protein-tyrosine-p
39 420 35.8 1499 2 I50212 protein-tyrosine-p
40 419.5 35.7 1175 2 S51005 protein-tyrosine-p
41 419 35.7 1291 1 A28334 protein-tyrosine-p
42 419 35.7 1304 1 A46346 leukocyte common a
43 418 35.6 435 1 TPHUN1 protein-tyrosine-p
44 416 35.4 1189 1 JC2366 protein-tyrosine-p
45 415.5 35.4 2314 1 A46151 protein-tyrosine-p

ALIGNMENTS

RESULT 1

T08716

protein-tyrosine-phosphatase homolog DKFZp566K0524.1 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C/Accession: T08716

submitted to the Protein Sequence Database, May 1999

A:Reference number: Z16472

A/Accession: T08716

A/Molecule type: mRNA

A/Residues: 1-398 <RNA>

A/Cross-references: UNIPROT:Q9Y406; EMBL:AL050040

A/Experimental source: fetal kidney; clone DKFZp566K0524

C:Genetics:

A/Note: DKFZp566K0524.1

F:161-379/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 79.0%; Score 928; DB 2; Length 398;
Best Local Similarity 77.9%; Pred. No. 2.4e-79;
Matches 169; Conservative 24; Mismatches 24; Indels 0; Gaps 0;

QY 2 NRDKNRYRDLPYDSTRVPLGKNKYINASYIRIVNHEEYFYIATQGPLPETIEDFWQM 61

Db 161 NREKNRYRDLPYDSTRVPLGKSKDYINASYIRIVNCGEEFYIATQGPLLSTIDDFWQM 220

QY 62 VLENNCNVIAITRETECGVIKCYSVMPISLKEPLFEHFSVLETFHTVQYFTRVFOI 121

Db 221 VLENNCNVIAITREMEGGIICVHYWPISLKKPLSKHFRVLENYQILQYFIIRFQV 280

QY 122 VKKSTGKSCVXHLQFTKWPDHGTTPASADFFIKYVYVRKSHITGPLLVCAGVGRGV 181

Db 281 VEKSTGTSVSHVQLQFTKWPDHGTTPASADSFYKIRYARKSHLTGPMVHCAGIGRTGV 340

QY 182 FICVDVWFSAIKENVSFDIMNIVTQMKQRCGMIOYK 218

Db 341 FLCVDVWFCAIVKDCSFNIMDIVAQMREQRSGMVQTK 377

RESULT 2

S71625

protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 13 - mouse

N/Alternate names: epidermal growth factor-binding protein; serine proteinase

C:Species: Mus musculus (house mouse)

C>Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004

C/Accession: S71625; S67987; I81210; I81209; S40290

R/Child: D.; Kume, T.; Mukoyama, Y.; Tabata, S.; Nomura, N.; Thomas, M.L.; Watanabe, T

FEBS Lett. 358, 233-239, 1995

A/Title: Characterization of a protein tyrosine phosphatase (RIP) expressed at a very ea

A/Reference number: S71625; MUID:95145716; PMID:7843407

A/Accession: S71625

A/Molecule type: mRNA

C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004

C/Accession: I67630
 R/Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
 FEBS Lett. 337, 200-206, 1994
 A>Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane
 A/Reference number: I53483; MUID:94116679; PMID:8287977
 A/Accession: I67630
 A/Status: Preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-2294 <RES>
 A/Cross-references: UNIPROT:Q12923; GB:D21211; NID:9452193; PIDN:BAA04752.1; PID:9452194
 C/Superfamily: protein-tyrosine phosphatase, nonreceptor type 13; GLGF domain homology;
 C/Keywords: phosphoric monoester hydrolase
 F:574-868/Domain: protein 4.1 membrane-binding domain homology <B41>
 F:1182-1258/Domain: GLGF domain homology <GLG2>
 F:2046-2265/Domain: protein-tyrosine-phosphatase homology <PTP>
 Query Match 46.1%; Score 541.5; DB 2; Length 2294;
 Best Local Similarity 47.0%; Pred. No. 3.6e-42;
 Matches 103; Conservative 37; Mismatches 78; Indels 1; Gaps 1;
 QY 1 QNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
 DB 2045 ENRRKNRYKNLLPYDATRVLPLGDEGGYINAFIKIPVGEKFVYIACQGLPTTVGDFWQ 2104
 QY 61 MVLNNCNVIAITREIECGVIKCYSWPISL-KEPFEHFSVFLTEHTVQYFTVRVF 119
 DB 2105 MIWEQKSTVIAMMTQVEGEKIKQRYWENILGKTWVSNRLRLALVRMQLKGFVVRAM 2164
 QY 120 QIVKSTGKSCVXHLQFTKPDHGTTPASADFFIKYVYVRKSHITGPLLHVSAGVGR 179
 DB 2165 TLEDIQTEVRHISHLNFTAWPDHDTFSQPDLLTTSYMRHHRSGPIITHCSAGIGRS 2224
 QY 180 GVPICVDFVFSAEKKNYSFDIMNIVTQMRKQRCGMIOTK 218
 DB 2225 GTLICIDVVLGLISQDLDFDISLVRMQLRQHGVMQTE 2263

RESULT 4

I67629

protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 2
 C/Species: Homo sapiens (man)
 C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
 C/Accession: I67629
 R/Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
 FEBS Lett. 337, 200-206, 1994
 A>Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membran
 A/Reference number: I53483; MUID:94116679; PMID:8287977
 A/Accession: I67629
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-2466 <RES>
 A/Cross-references: UNIPROT:Q12923; GB:D21210; NID:9452191; PIDN:BAA04751.1; PID:945219
 C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
 C/Keywords: phosphoric monoester hydrolase
 F:574-868/Domain: protein 4.1 membrane-binding domain homology <B41>
 F:1354-1430/Domain: GLGF domain homology <GLG2>
 F:2218-2437/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 46.1%; Score 541.5; DB 2; Length 2466;
 Best Local Similarity 47.0%; Pred. No. 3.9e-42;
 Matches 103; Conservative 37; Mismatches 78; Indels 1; Gaps 1;

QY 1 QNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60

DB 2217 ENRRKNRYKNLLPYDATRVLPLGDEGGYINAFIKIPVGEKFVYIACQGLPTTVGDFWQ 2276

QY 61 MVLNNCNVIAITREIECGVIKCYSWPISL-KEPFEHFSVFLTEHTVQYFTVRVF 119

DB 2277 MIWEQKSTVIAMMTQVEGEKIKQRYWENILGKTWVSNRLRLALVRMQLKGFVVRAM 2336

QY 120 QIVKSTGKSCVXHLQFTKPDHGTTPASADFFIKYVYVRKSHITGPLLHVSAGVGR 179

DB 2277 MIWEQKSTVIAMMTQVEGEKIKQRYWENILGKTWVSNRLRLALVRMQLKGFVVRAM 2336

QY 120 QIVKSTGKSCVXHLQFTKPDHGTTPASADFFIKYVYVRKSHITGPLLHVSAGVGR 179

DB 2277 MIWEQKSTVIAMMTQVEGEKIKQRYWENILGKTWVSNRLRLALVRMQLKGFVVRAM 2336

QY 120 QIVKSTGKSCVXHLQFTKPDHGTTPASADFFIKYVYVRKSHITGPLLHVSAGVGR 179

DB 2277 MIWEQKSTVIAMMTQVEGEKIKQRYWENILGKTWVSNRLRLALVRMQLKGFVVRAM 2336

QY 120 QIVKSTGKSCVXHLQFTKPDHGTTPASADFFIKYVYVRKSHITGPLLHVSAGVGR 179

DB 2277 MIWEQKSTVIAMMTQVEGEKIKQRYWENILGKTWVSNRLRLALVRMQLKGFVVRAM 2336

A/Residues: 1-2450 <CHI>
 A/Cross-references: UNIPROT:Q64512; UNIPROT:Q62370; EMBL:D83966; NID:g12322103; PIDN:BRA1
 A/Experimental source: strain DBA/2; cell line MEL 7454
 R/Wolf, B.B.; Brown, M.D.
 FEBS Lett. 376, 177-180, 1995
 A>Title: Epidermal growth factor-binding protein activates soluble and receptor-bound si
 A/Reference number: S67987; MUID:96105375; PMID:7498536
 A/Accession: S67987
 A/Molecule type: protein
 A/Residues: 1098-1102 <WOL>
 A/Experimental source: submaxillary glands
 R/Sato, T.; Irie, S.; Kitada, S.; Reed, J.C.
 Science 268, 411-415, 1995
 A>Title: PAP-1: a protein tyrosine phosphatase that associates with Fas.
 A/Reference number: I59595; MUID:95232528; PMID:7536343
 A/Accession: I81210
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1338-1354, K', 1356-1447, R', 1449-1454 <RE2>
 A/Cross-references: GB:I34581; NID:9806295; PIDN:AAC42055.1; PID:g806296
 R/Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
 submitted to the EMBL Data Library, June 1993
 A/Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
 A/Reference number: S40280
 A/Accession: S40290
 A/Molecule type: mRNA
 A/Residues: 2266-2372 <HEN>
 A/Cross-references: EMBL:Z23059; NID:g438155; PIDN:CAA80594.1; PID:g438156
 C/Genetics:
 A/Gene: Ptpn13
 A/Map position: 5
 C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
 C/Keywords: phosphoprotein; phosphoric monoester hydrolase; transmembrane protein; tyro
 F:566-860/Domain: protein 4.1 membrane-binding domain homology <B41>
 F:1089-1165/Domain: GLGF domain homology <GLG1>
 F:1361-1437/Domain: GLGF domain homology <GLG2>
 F:1495-1574/Domain: GLGF domain homology <GLG3>
 F:1769-1840/Domain: GLGF domain homology <GLG4>
 F:1863-1937/Domain: GLGF domain homology <GLG5>
 F:2203-2422/Domain: protein-tyrosine-phosphatase homology <PTP1>
 F:2374/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:2380/Binding site: substrate phosphate (Arg) #status predicted
 Query Match 46.6%; Score 547.5; DB 2; Length 2450;
 Best Local Similarity 49.1%; Pred. No. 1.1e-42;
 Matches 109; Conservative 35; Mismatches 71; Indels 7; Gaps 3;

QY 1 QNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60

DB 2202 ENRRKNRYKNLLPYDSTRVPLGDEGGYINAFIRIPVGTQFVYIACQGLPTTVGDFWQ 2261

QY 61 MVLNNCNVIAITREIECGVIKCYSWPISL-KEPFEHFSVFLTEHTVQYFTVRVF 119

DB 2262 MVWEQNSTVIAMMTQVEGEKIKQRYWENILGKTWVSNRLRLALVRMQLKGFVVRAM 2321

QY 120 QIVKSTGKSCVXHLQFTKPDHGTTPASAD---PFIKYVYVRKSHITGPLLHVSAGV 176

DB 2322 ALEDIQTEVRHISHLNFTAWPDHDTFSQPDLLTTSYMRHHRSGPIITHCSAGI 2378

QY 177 GRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOTK 218

DB 2379 GRSGLTICIDVVLGLISQDLDFDISLVRMQLRQHGVMQTE 2420

QY 177 GRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOTK 218

DB 2379 GRSGLTICIDVVLGLISQDLDFDISLVRMQLRQHGVMQTE 2420

QY 177 GRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOTK 218

DB 2379 GRSGLTICIDVVLGLISQDLDFDISLVRMQLRQHGVMQTE 2420

QY 177 GRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOTK 218

DB 2379 GRSGLTICIDVVLGLISQDLDFDISLVRMQLRQHGVMQTE 2420

QY 177 GRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOTK 218

DB 2379 GRSGLTICIDVVLGLISQDLDFDISLVRMQLRQHGVMQTE 2420

QY 177 GRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOTK 218

DB 2379 GRSGLTICIDVVLGLISQDLDFDISLVRMQLRQHGVMQTE 2420

QY 177 GRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOTK 218

DB 2379 GRSGLTICIDVVLGLISQDLDFDISLVRMQLRQHGVMQTE 2420

QY 177 GRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOTK 218

DB 2379 GRSGLTICIDVVLGLISQDLDFDISLVRMQLRQHGVMQTE 2420

QY 177 GRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOTK 218

C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004
C:Accession: S17671; S40287
R:Gebblink, M.F.B.G.; van Etten, I.; Hateboer, G.; Suijkerbuijk, R.; Beijersbergen, R.L.; FBS Lett. 290, 123-130, 1991
A:Title: Cloning, expression and chromosomal localization of a new putative receptor-like A:Reference number: S17669; MUID:92008644; PMID:1655529
A:Accession: S17671
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-583 <GEN>
A:Cross-references: UNIPROT:Q64497; EMBL:X58289
R:Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
submitted to the EMBL Data Library, June 1993
A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatases A:Reference number: S40280
A:Molecule type: mRNA
A:Residues: 377-483, 'T', 485-486 <GEN>
A:Cross-references: EMBL:223056; NID:G438150
C:Superfamily: protein-tyrosine-phosphatase, receptor type beta; fibronectin type III re C:Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane prot F:311-536/Domain: protein-tyrosine-phosphatase homology <PTP>
F:488/Active site: Cys (phosphocysteine intermediate) #status predicted
F:494/Binding site: substrate phosphate (Arg) #status predicted
Query Match 38.2%; Score 448.5; DB 2; Length 583;
Best Local Similarity 41.2%; Pred. No. 3.8e-34;
Matches 94; Conservative 40; Mismatches 81; Indels 13; Gaps 5;
QY 1 QNRDKNRYDILPYDSTRVPLGK----NKDYINASYIRIVNHEEYFYIATGGLPETI 55
DB 310 ENRKNRYNNILPYDSTRVPLGK----NKDYINASYIRIVNHEEYFYIATGGLPETI 55
QY 56 EDFQWVLENNCNVIAITREIECGVICKYVWPISLKEPFEHFSVLETFHVTQYFT 115
DB 368 DDFKMWAEQVNHVIMVTQVCKGRVKCDHYWPAQ-QDPLYYGDLILQVLSVLPET 426
QY 116 VRVQIV-KKSTGKSCVQKHLQFTKWDHGTASADFFIKYVR-----YVRKSHITGPLL 170
DB 427 IREFKICSEQLDAHLRLIRHFHYTVPDGHGVPETTSQSLQFVTRVDYINRSPGAGPSV 486
QY 171 HCSAGVGRGTGVTCDVDFVSAIEKNYSFDIMNVTOMRKORCGMIOTK 218
DB 487 HCSAGVGRGTGVTCDVDFVSAIEKNYSFDIMNVTOMRKORCGMIOTK 218
RESULT 8
S12050
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type beta precursor - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S12050; S15818; S15819
R:Krueger, N.X.; Streuli, M.; Saito, H.
EMBO J. 9, 3241-3252, 1990
A:Title: Structural diversity and evolution of human receptor-like protein tyrosine phos A:Reference number: S12049; MUID:9106018; PMID:2170109
A:Accession: S12050
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1997 <KRU>
A:Cross-references: UNIPROT:P23467; GB:X54131; NID:G35787; PIDN:CAA38066.1; PID:G35788
R:de Vries, L.; Li, R.Y.; Ragab, A.; Ragab-Thomas, J.M.F.; Chap, H.
FEBS Lett. 282, 285-288, 1991
A:Title: Expression of a truncated protein-tyrosine phosphatase mRNA in human lung.
A:Reference number: S15818; MUID:91243813; PMID:1645282
A:Accession: S15818
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1872-1911, 'VHMVLQK' <VRI>
A:Accession: S15819
A:Status: not compared with conceptual translation
A:Molecule type: mRNA

A:Residues: 1872-1997 <VR2>
C:Genetics:
A:Gene: GDB:PTPRB; PTPB
A:Cross-references: GDB:127352; OMIM:176882
A:Map position: 12q15-12q21
C:Superfamily: protein-tyrosine-phosphatase, receptor type beta; fibronectin type III re C:Keywords: alternative splicing; signal sequence #status predicted <SIG>
F:1-22/Domain: protein-tyrosine-phosphatase, receptor type beta #status predicted <EXT>
F:23-1997/Product: protein-tyrosine-phosphatase, receptor type beta #status predicted <EXT>
F:23-1625/Domain: extracellular #status predicted <EXT>
F:1626-1642/Domain: transmembrane #status predicted <TMM>
F:1643-1997/Domain: intracellular #status predicted <INT>
F:1727-1952/Domain: protein-tyrosine-phosphatase homology <PTP>
F:1904/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1910/Binding site: substrate phosphate (Arg) #status predicted
Query Match 37.9%; Score 445.5; DB 1; Length 1997;
Best Local Similarity 41.7%; Pred. No. 3.1e-33;
Matches 95; Conservative 38; Mismatches 82; Indels 13; Gaps 5;
QY 1 QNRDKNRYDILPYDSTRVPLGK----NKDYINASYIRIVNHEEYFYIATGGLPETI 55
DB 1726 ENRKNRYNNILPYDSTRVPLGK----NKDYINASYIRIVNHEEYFYIATGGLPETI 55
QY 56 EDFQWVLENNCNVIAITREIECGVICKYVWPISLKEPFEHFSVLETFHVTQYFT 115
DB 1784 DDFKMWAEQVNHVIMVTQVCKGRVKCDHYWPAQ-QDPLYYGDLILQVLSVLPET 1842
QY 116 VRVQIV-KKSTGKSCVQKHLQFTKWDHGTASADFFIKYVR-----YVRKSHITGPLL 170
DB 1843 IREFKICSEQLDAHLRLIRHFHYTVPDGHGVPETTSQSLQFVTRVDYINRSPGAGPTV 1902
QY 171 HCSAGVGRGTGVTCDVDFVSAIEKNYSFDIMNVTOMRKORCGMIOTK 218
DB 1903 HCSAGVGRGTGVTCDVDFVSAIEKNYSFDIMNVTOMRKORCGMIOTK 218
RESULT 9
A41105
protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN4, nonreceptor type 4 [validated] - human
N:Alternate names: PTPase MEG
C:Species: Homo sapiens (man)
C:Date: 20-Mar-1992 #sequence_revision 02-May-1994 #text_change 09-Jul-2004
C:Accession: A41105
R:Gu, M.; York, J.D.; Warshawsky, I.; Majerus, P.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 5867-5871, 1991
A:Title: Identification, cloning, and expression of a cytosolic megakaryocyte protein-ty A:Reference number: A41105; MUID:91288564; PMID:1648233
A:Accession: A41105
A:Molecule type: mRNA
A:Residues: 1-926 <GUA>
A:Cross-references: UNIPROT:P29074; GB:M68941; NID:G190747; PIDN:AAA36530.1; PID:G190747
A:Experimental source: megakaryocytes, cell line MEG-10
C:Genetics:
A:Gene: GDB:PTPN4
A:Cross-references: GDB:131387; OMIM:176878
A:Map position: 9q31-9q31
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology; p C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase F:31-308/Domain: protein 4.1 membrane-binding domain homology <B41>
F:523-597/Domain: GLGF domain homology <GLG>
F:679-900/Domain: protein-tyrosine-phosphatase homology <PTP>
F:852/Active site: Cys (phosphocysteine intermediate) #status predicted
F:858/Binding site: substrate phosphate (Arg) #status predicted
Query Match 37.9%; Score 444.5; DB 1; Length 926;
Best Local Similarity 41.0%; Pred. No. 1.6e-33;
Matches 94; Conservative 35; Mismatches 79; Indels 21; Gaps 5;
QY 1 QNRDKNRYDILPYDSTRVPLGKNKYINASYIR-----IVNHEEYFYIATGGLPE 53
DB 678 QNISKRYRDISPYDSTRVPLGKNKYINASYIR-----IVNHEEYFYIATGGLPE 53

QY 54 TIEDEFQWVLENNCNVMIATREIECGVVKCYWPIISLKEPLEFHFVSVFLETHVTVQY 113
 Db 733 TCTDFQWMTWEGSSNMVMTLTQVERGRVKCHQYWP-----EPTGSSYCYQVTVCHSERG 788
 QY 114 FTVRVVFQ-----IVKSTGKSCQCVKHLQFTKWPDPHGTPASADFFIKYVYRKSHI--TGPL 168
 Db 789 NTAYIFRKMTLNFQEKESRPLTQIYIAPDGHGVDDSSDLDFVCHVNRKRAKEEPV 848
 QY 169 LVHCSAGVORTGVFICVDVVFSAIEKNYSFDMNIVTQMRKORCGMIQT 217
 Db 849 VVHCSAGIGRTGVLITMETRYAMCLIECNQVPYPLDIVRTMRDQRAMMIQT 897

RESULT 10
 138670
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type J precursor - human
 N:Alternate names: density enhanced phosphatase-1 (DEP-1); protein-tyrosine phosphatase
 C:Species: Homo sapiens (man)
 C>Date: 01-Mar-1996 #sequence_revision 08-Mar-1996 #text_change 09-Jul-2004
 C:Accession: I38670; MUID:95024024; PMID:7937872
 R:Ostman, A.; Yang, Q.; Tonks, N.K.
 Proc. Natl. Acad. Sci. U.S.A. 91, 9680-9684, 1994
 A:Title: Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, is enhanced
 A:Reference number: I38670; MUID:95024024; PMID:7937872
 A:Accession: I38670
 A:Molecule type: mRNA
 A:Residues: 1-1337 <RES>
 A:Cross-references: UNIPROT:Q12913; EMBL:U01886; NID:G558754; PID:G558755
 A:Experimental source: HeLa cells
 R:Honda, H.; Inazawa, J.; Nishida, J.; Yazaki, Y.; Hirai, H.
 Blood 84, 4186-4194, 1994
 A:Title: Molecular cloning, characterization, and chromosomal localization of a novel pr
 A:Reference number: I52599; MUID:95086212; PMID:7994032
 A:Accession: I52599
 A:Status: preliminary; translated from GB/EMBL/DBDJB
 A:Molecule type: mRNA
 A:Residues: 1-216; 'LTGVKKA', 225-260, 'G', 262-285, 'GTGGGLDASNTSRRA', 302, 'S', 304, 'TAPVHDE
 A:Cross-references: GB:D37781; NID:9633072; PIDN:BAA07035.1; PID:9633073
 C:Comment: Enhanced expression of this protein with increasing cell density suggests a
 C:Genetics:
 A:Gene: GDB:PTPRJ
 A:Cross-references: GDB:385040; OMIM:600925
 A:Map position: 19ql3.4-19ql3.4
 C:Function:
 A:Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and
 C:Superfamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III repea
 C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; receptor; tran
 F:1-35/Domain: signal sequence #status predicted <SIG>
 F:36-1337/Product: protein-tyrosine-phosphatase, receptor type J #status predicted <MAT>
 F:118-197/Domain: fibronectin type III repeat homology <3FNA>
 F:206-283/Domain: fibronectin type III repeat homology <3FNB>
 F:284-356/Domain: fibronectin type III repeat homology #status atypical <3FNC>
 F:365-445/Domain: fibronectin type III repeat homology <3FND>
 F:453-530/Domain: fibronectin type III repeat homology <3FNE>
 F:539-617/Domain: fibronectin type III repeat homology <3FNF>
 F:720-804/Domain: fibronectin type III repeat homology <3FNG>
 F:972-986/Domain: fibronectin type III repeat homology <3FNG>
 F:972-986/Domain: transmembrane #status predicted <TMN>
 F:1065-1287/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:72, 82, 93, 104, 142, 172, 192, 231, 258, 278, 342, 351, 376, 391, 396, 413, 431, 501, 525, 536, 582, 603, 6
 F:1239/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1245/Binding site: substrate phosphate (Arg) #status predicted

Query Match 37.8%; Score 444; DB 1; Length 1337;
 Best Local Similarity 41.2%; Pred. No. 2,7e-33;
 Matches 93; Conservative 42; Mismatches 79; Indels 12; Gaps 5;

QY 1 QNRDKNRYRDLIPYDSTRVPLG----KNDYINASYIRIVNHEEYFYIATOGPLPETIE 56
 Db 1064 ENRKRNRYNNVLPYDSTRVPLG-----KNDYINASYIRIVNHEEYFYIATOGPLPETIE 56

QY 57 DFWQVLENNCNVMIATREIECGVVKCYWPIISLKEPLEFHFVSVFLETHVTVQY 116
 Db 1122 DFWRMWKNVYAIIMLTKEVGRKCEYWP--SKQADYGDIIIVMTSEIVLPETWI 1179

QY 117 RVFQIVKSTGKSCQCVKHLQFTKWPDPHGTPASADFFIKY---VR-YVRKSHITGPLLVC 172
 Db 1180 RDTFQWMTWEGSSNMVMTLTQVERGRVKCHQYWP-----EPTGSSYCYQVTVCHSERG 1239
 QY 173 SAGVORTGVFICVDVVFSAIEKNYSFDMNIVTQMRKORCGMIQT 218
 Db 1240 SAGVORTGVFICVDVVFSAIEKNYSFDMNIVTQMRKORCGMIQT 1285

RESULT 11
 T30938
 receptor tyrosine phosphatase - medicinal leech
 C:Species: Hirudo medicinalis (medicinal leech)
 C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T30938
 R:Gershon, T.R.; Baker, M.; Nitabach, M.; Wu, P.; Macagno, E.R.
 submitted to the EMBL Data Library, December 1997
 A:Description: Two receptor tyrosine phosphatases of the LAR subfamily are expressed in
 A:Reference number: Z20939
 A:Accession: T30938
 A:Status: preliminary; translated from GB/EMBL/DBDJB
 A:Molecule type: mRNA
 A:Residues: 1-2051 <GER>
 A:Cross-references: UNIPROT:O44328; EMBL:AF017083; NID:G2695654; PID:G2695655; PIDN:AA89
 C:Genetics:
 A:Gene: LAR2
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
 ogy

Query Match 37.3%; Score 437.5; DB 2; Length 2051;
 Best Local Similarity 39.6%; Pred. No. 1.8e-32;
 Matches 90; Conservative 45; Mismatches 77; Indels 15; Gaps 6;

QY 2 NRDKNRYRDLIPYDSTRVPLG----KNDYINASYIRIVNHEEYFYIATOGPLPETIE 56
 Db 1808 NKQKRLNVLPYETTRVCLQPIRGVDSYINASFID--GYRPRAYIATOGPLPETIE 1865
 QY 57 DFWQVLENNCNVMIATREIECGVVKCYWPIISLKEPLEFHFVSVF-LETHVTVQYPT 115
 Db 1866 DFWRALWESNCNIIVMTKLRMGREMCQYWP--SERSARYQYFVVDPLAENVMPQYI- 1922

QY 116 RVFQIVKSTGKSCQCVKHLQFTKWPDPHGTPASADFFIKYVYRKSH---ITGPLLVC 171
 Db 1923 LREFFQVSDARDQSRMTMRQFQUTDMPQGVPTDGFIDFQGTHTKTKESFGQEGEIVAH 1982

QY 172 CSAGVORTGVFICVDVVFSAIEKNYSFDMNIVTQMRKORCGMIQT 218
 Db 1983 CSAGVORTGVFICVDVVFSAIEKNYSFDMNIVTQMRKORCGMIQT 2029

RESULT 12
 A38191
 protein-tyrosine-phosphatase (EC 3.1.3.48) 11A - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Feb-1994 #sequence_revision 02-May-1994 #text_change 09-Jul-2004
 C:Accession: A38191
 R:Mosinger Jr., B.; Tillmann, U.; Westphal, H.; Tremblay, M.L.
 Proc. Natl. Acad. Sci. U.S.A. 89, 499-503, 1992
 A:Title: Cloning and characterization of a mouse cDNA encoding a cytoplasmic protein-ty
 A:Reference number: A38191; MUID:92115688; PMID:1731319
 A:Accession: A38191
 A:Molecule type: mRNA
 A:Residues: 1-382 <MOS>
 A:Cross-references: UNIPROT:Q06180; GB:M81477; NID:G192683; PIDN:AAA37446.1; PID:G192684
 A:Note: sequence extracted from NCBI backbone (NCBIIN:75809, NCBIIP:75812)
 C:Comment: This transcript was found in a variety of embryonic and adult tissues. A shor
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type I; protein-tyrosine-phosph
 C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyros
 F:42-264/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:216/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:222/Binding site: substrate phosphate (Arg) #status predicted

Query Match 37.1%; Score 436; DB 1; Length 382;
Best Local Similarity 40.4%; Pred. No. 3.4e-33;
Matches 90; Conservative 38; Mismatches 87; Indels 8; Gaps 4;

QY 1 QNRDKNRYRDLPYDSTRVPL-GKKNDKYNASYIRIVNHHEEYFYIATQGRLPETIEDFW 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 41 ENRNENRYRDSVPDHRSVKLQSTENDYINASLVDI--EEAQRSYLITQGRLPNTCCHF 98
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 60 QMWLENNCNVLAMITRETECGVIKCYSWMPISLKEPLBPE-HFSVFLETFFHTQVFTVRV 118
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 99 LMVVOQKTAVVMNLNRTVEKESVKAQWPTDDREWFVKETGFSVKLLSEDVKSYTVHL 158
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 FQIVKSKTGSCQVKHLOFTKPWDHGTPASADFFIKYRVYRKSHIT----GLILVHC 174
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 159 LQLENINTGETTISHFHYTTWPDFGVBPSPASFNLFLPKVRESGCLTDPHGPVATHCS 218
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 175 GVGRGTGVCVDVVSFAIEKNYSFDIMNIVTOMRKQRCEMIQT 217
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 219 GIGRGSTSLVDTCILVMEKGEDVANVQLLNRRKYRMGLIQT 261
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13

S68700
HPTTP beta-like tyrosine phosphatase precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68700
S:Kuramochi, S.; Matsuda, S.; Matsuda, Y.; Satoh, T.; Ohsugi, M.; Yamamoto, T.
FEBBS Lett. 378, 7-14, 1996
A:Title: Molecular cloning and characterization of Byx, a murine receptor-type tyrosine kinase cDNA.
A:Reference number: S68700; MUID:96140699; PMID:8549806
A:Accession: S68700
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1238 <CUR>
A:Cross-references: UNIPROT:Q64455; GB:D45212; NID:g1208432; PID:BAA08146.1; PID:g1208432
C:Genetics:
A:Map position: 2E1-2
C:Superfamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III repeat type I
C:Keywords: phosphoprotein
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-1238/Product: HPTP beta-like tyrosine phosphatase #status predicted <MAT>
F:267-347/Domain: fibronectin type III repeat homology <3FR>
F:966-1186/Domain: protein-tyrosine-phosphatase homology <PTP>
F:1140/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1146/Binding site: substrate phosphate (ARG) #status predicted

Query Match 37.1%; Score 436; DB 2; Length 1238;
Best Local Similarity 39.6%; Pred. No. 1.4e-32;
Matches 90; Conservative 43; Mismatches 80; Indels 14; Gaps 5;

QY 1 QNRDKNRYRDLPYDSTRVPLG---KNKDYNASYIRIVNHHEEYFYIATQGLPETIE 56
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 965 ENRGKNRYNVLPDISRVLSVQTHSDTDINANYMPPGVHSKKD--FIATQGLPLETK 1022
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 57 DFMQWLNNNCNVIAMITREIECGVICYSWPISLKEPLFEHFSVLETFHTVQVFTV 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1023 DFRWNWKNVYAIVMLTKVEQGRYKCEYWP--SKQAQYGDITVAMTSEVLPBWTI 1080
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 117 RVFQIVKSKTGSCQVKHLOFTKPWDHGTPASADFFIKYRVYRKSHI-----TGPLLHV 171
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1081 RDPVNMNQNSGHPLRQPFTSWPDHGVPDTDDLINF-RYLVRDYMKQIPPEPSILVH 1139
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 172 CSAGVGRTGVFCVDVVFSIAEKSNYSFDIMNIVTOMRKQRCEMIOTK 218
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1140 CSAGVGRTGFIAIDLRIYQIENENTVDVYGIVYDLNRHRLMVQTE 1186
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14

A60345
protein-tyrosine-phosphatase (EC 3.1.3.48) 11a - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1993 #sequence_revision 02-May-1994 #text_change 24-Apr-1998

C;Accession: A60345; B60345
R;Champion-Arnoud, P.; Gesnel, M.C.; Foulkes, N.; Ronsin, C.; Sassone-Corsi, P.; Breath
Oncogene 6, 1203-1209, 1991
A;Title: Activation of transcription via AP-1 or CREB regulatory sites is blocked by pro
A;Reference number: A60345; MUID:91319401; PMID:1650442
A;Accession: A60345
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-387 <CHA>
A;Accession: B60345
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 348-387 <CH2>
C;Genetics:
A;Gene: GDB:PTPN2; PTPT
A;Cross-references: GDB:128098; OMIM:176887
A;Map position: 18p11.22-19p11.21
A;Introns: 347/2; 381/2
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 1; protein-tyrosine-phosph
C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosi
F;42-264/Domain: protein-tyrosine-phosphatase homology <PTP>
F;216/Active site: Cys (phosphocysteine intermediate) #status predicted
F;222/Binding site: substrate phosphate (Arg) #status predicted

Query Match 37.1%; Score 435; DB 1; Length 387;
Best Local Similarity 40.9%; Pred. No. 4.3e-33;
Matches 92; Conservative 37; Mismatches 84; Indels 12; Gaps 5;

Qy 1 QNKKRKYRILYDSTRVPL-GKNKDYINASVIRVNHHEEYFYIATGGLPETIEDFW 59
Db 41 ENNRNRYDVSYPDSHRVKVQLNAENDYINASLVDI--EAAQSYILTOGLPLNTCCHF 98
Qy 60 QWLNNCNVIAITTEIEGCVTKCYSYNPISLKEPLEFE-HFSVFLETFHVYQYETVRV 118
Db 99 LMWQQTAKAVMLNRIVEKSVKCAQYPTDDQMLFKETGFSVKLLSDEVKSYVTVHL 158
Qy 119 FQIVKSKTGKQCCKHLOFTKWPDHGTPASADFFIKYRVYRKSS-----HITGPLLHVC 172
Db 159 LQLENINSGETRTISHFYTTTDPDGVPEPASFNLFLFKVRESGSLNPDH--GPAVICH 216
Qy 173 SAGVGRGVFICVDVVPFSAEKKNYSFDIMNVQMRKQRCGMIOQT 217
Db 217 SAGIGRSGTFYLVDTCLVLMKEGDINIKQVLLNMRKYMGLIOQT 261

RESULT 15
SI4294
protein-tyrosine-phosphatase (EC 3.1.3.48) 11A - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: SI4294; S21831
R;Swarup, G.; Kamatkar, S.; Radha, V.; Rema, V.
FEBS Lett. 280, 65-69, 1991
A;Title: Molecular cloning and expression of a protein-tyrosine phosphatase showing hom
A;Reference number: SI4294; MUID:91184422; PMID:1849097
A;Accession: SI4294
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-363 <SWA>
A;Cross-references: UNIPROT:P35233; GB:X58828; NID:g56995; PIDN:CAA41633.1; PID:g56996
R;Swarup, G.; Kamatkar, S.; Radha, V.; Rema, V.
submitted to the EMBL Data Library, April 1991
A;Reference number: S21831
A;Accession: S21831
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-363 <SWA2>
A;Cross-references: EMBL:X58828; NID:g56995; PIDN:CAA41633.1; PID:g56996
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 1; protein-tyrosine-phosp
C;Keywords: alternative splicing; DNA binding; phosphoprotein; phosphoric monoester hyd
F;42-264/Domain: protein-tyrosine-phosphatase homology <PTP>
F;216/Active site: Cys (phosphocysteine intermediate) #status predicted
F;222/Binding site: substrate phosphate (Arg) #status predicted

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 1, 2004, 12:16:33 ; Search time 397.117 Seconds
(without alignments)
195.771 Million cell updates/sec

Title: US-09-095-478a-7_COPY_188_405

Perfect score: 1174

Sequence: 1 QNRDKNRYRDLIPYDSTRVP.....DIMNIVTQMRKQRCGMIOYK 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pap.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pap.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pap.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pap.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pap.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pap.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pap.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pap.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pap.*
12: /cgn2_6/ptodata/2/pubpaa/US09C_NEW_PUB.pap.*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pap.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pap.*
16: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pap.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pap.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1174	100.0	354	10	US-09-095-478-6
2	1174	100.0	379	10	US-09-095-478-8
3	1174	100.0	412	10	US-09-095-478-3
4	1174	100.0	426	10	US-09-095-478-1
5	1174	100.0	463	10	US-09-095-478-2
6	936	79.7	420	15	US-10-311-764-4
7	668	56.9	122	10	US-09-095-478-4
8	566	48.2	122	10	US-09-095-478-5
9	550.5	46.9	381	10	US-09-095-478-7
10	541.5	46.1	358	10	US-09-095-478-9
11	541.5	46.1	1267	14	US-10-060-065-35
12	541.5	46.1	1267	14	US-10-059-585-56
13	541.5	46.1	2466	14	US-10-177-980-12

14 541.5 46.1 2466 17 US-10-795-148-2 Sequence 2, Appli
15 541.5 46.1 2485 9 US-09-802-669-46 Sequence 46, Appl
16 541.5 46.1 2485 15 US-10-619-220-46 Sequence 46, Appl
17 541.5 46.1 2485 16 US-10-408-765A-1349 Sequence 1349, Ap
18 524 44.6 263 15 US-10-087-684-93 Sequence 93, Appl
19 524 44.6 263 15 US-10-218-779-93 Sequence 93, Appl
20 499 42.5 235 15 US-10-087-684-94 Sequence 94, Appl
21 499 42.5 235 15 US-10-218-779-94 Sequence 94, Appl
22 499 42.5 235 15 US-10-072-012-819 Sequence 819, Appl
23 467 39.8 703 14 US-10-366-547-40 Sequence 40, Appl
24 467 39.8 913 9 US-09-848-294-2 Sequence 2, Appli
25 467 39.8 913 14 US-10-293-231-2 Sequence 2, Appli
26 467 39.8 913 14 US-10-366-547-38 Sequence 38, Appl
27 462 39.4 244 9 US-09-848-294-7 Sequence 7, Appli
28 462 39.4 244 14 US-10-293-231-7 Sequence 7, Appli
29 456 38.8 291 9 US-09-788-626-22 Sequence 22, Appl
30 445.5 37.9 312 15 US-10-634-027-6 Sequence 6, Appli
31 445.5 37.9 319 15 US-10-634-027-7 Sequence 7, Appli
32 445.5 37.9 336 15 US-10-634-027-4 Sequence 4, Appli
33 445.5 37.9 1397 10 US-09-909-567B-54 Sequence 54, Appl
34 445.5 37.9 1997 15 US-10-634-027-2 Sequence 2, Appli
35 445.5 37.9 1997 16 US-10-408-765A-2135 Sequence 2135, Ap
36 444 37.8 341 16 US-10-723-606-3 Sequence 3, Appli
37 444 37.8 1337 14 US-10-390-501-2 Sequence 2, Appli
38 444 37.8 1337 14 US-10-366-547-42 Sequence 42, Appl
39 444 37.8 1337 14 US-10-366-547-44 Sequence 44, Appl
40 444 37.8 1337 16 US-10-723-606-2 Sequence 2, Appli
41 442.5 37.7 264 14 US-10-245-539-6 Sequence 6, Appli
42 437.5 37.3 1948 9 US-09-808-602-55 Sequence 55, Appl
43 437.5 37.3 1948 10 US-09-800-198-45 Sequence 45, Appl
44 437 37.2 1216 14 US-10-366-547-49 Sequence 49, Appl
45 436 37.1 382 14 US-10-366-547-22 Sequence 22, Appl

ALIGNMENTS

RESULT 1

US-09-095-478-6
; Sequence 6, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUPT05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
;
US-09-095-478-6

Query Match 100.0%; Score 1174; DB 10; Length 354;
Best Local Similarity 100.0%; Pred. No. 3.1e-119;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNRDKNRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
Db 118 QNRDKNRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 177
QY 61 MVLNNCNVMIATREIECGVIKCYSWPISLKEPFEHFSVLETFHVTQYFTVRVFQ 120
Db 178 MVLNNCNVMIATREIECGVIKCYSWPISLKEPFEHFSVLETFHVTQYFTVRVFQ 237
QY 121 IVKSTGKSCQVXHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLHVCAGVGRGTG 180
Db 238 IVKSTGKSCQVXHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLHVCAGVGRGTG 297
QY 181 VFICVDVVFSAIEKNYSFDMINIVTQMRKORCGMIQTK 218
Db 298 VFICVDVVFSAIEKNYSFDMINIVTQMRKORCGMIQTK 335

RESULT 2
US-09-095-478-8
; Sequence 8, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SuptP05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
;
US-09-095-478-8

Query Match 100.0%; Score 1174; DB 10; Length 379;
Best Local Similarity 100.0%; Pred. No. 3.4e-119;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNRDKNRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
Db 143 QNRDKNRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 202
QY 61 MVLNNCNVMIATREIECGVIKCYSWPISLKEPFEHFSVLETFHVTQYFTVRVFQ 120
Db 203 MVLNNCNVMIATREIECGVIKCYSWPISLKEPFEHFSVLETFHVTQYFTVRVFQ 262
QY 121 IVKSTGKSCQVXHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLHVCAGVGRGTG 180
Db 263 IVKSTGKSCQVXHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLHVCAGVGRGTG 322
QY 181 VFICVDVVFSAIEKNYSFDMINIVTQMRKORCGMIQTK 218
Db 323 VFICVDVVFSAIEKNYSFDMINIVTQMRKORCGMIQTK 360

RESULT 3
US-09-095-478-3
; Sequence 3, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SuptP05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
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```
;
; LENGTH: 412 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-09-095-478-3

Query Match 100.0%; Score 1174; DB 10; Length 412;
Best Local Similarity 100.0%; Pred. No. 3.8e-119;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNRDKNRYRDLIPYDSTRVPLGKKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
Db 188 QNRDKNRYRDLIPYDSTRVPLGKKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 247
Qy 61 MVLNNCNVIMITREIECGVIKCYSWPISLKEPFEHFSVLETFHVTQYFTVRVFQ 120
Db 248 MVLNNCNVIMITREIECGVIKCYSWPISLKEPFEHFSVLETFHVTQYFTVRVFQ 307
Qy 121 IVKSTGSKQCVKHLQFTKWPDHGTGPASADFFIKYVYVRKSHITGPLLHVCAGVGRGTG 180
Db 308 IVKSTGSKQCVKHLQFTKWPDHGTGPASADFFIKYVYVRKSHITGPLLHVCAGVGRGTG 367
Qy 181 VFICVDVWFSIAEKNSYFDMINIVTQMRKORCGMIQTK 218
Db 368 VFICVDVWFSIAEKNSYFDMINIVTQMRKORCGMIQTK 405

RESULT 4
US-09-095-478-1
; Sequence 1, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUPT05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

;
; MOLECULE TYPE: Peptide
; US-09-095-478-2

Query Match 100.0%; Score 1174; DB 10; Length 412;
Best Local Similarity 100.0%; Pred. No. 3.8e-119;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNRDKNRYRDLIPYDSTRVPLGKKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
Db 188 QNRDKNRYRDLIPYDSTRVPLGKKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 247
Qy 61 MVLNNCNVIMITREIECGVIKCYSWPISLKEPFEHFSVLETFHVTQYFTVRVFQ 120
Db 248 MVLNNCNVIMITREIECGVIKCYSWPISLKEPFEHFSVLETFHVTQYFTVRVFQ 307
Qy 121 IVKSTGSKQCVKHLQFTKWPDHGTGPASADFFIKYVYVRKSHITGPLLHVCAGVGRGTG 180
Db 308 IVKSTGSKQCVKHLQFTKWPDHGTGPASADFFIKYVYVRKSHITGPLLHVCAGVGRGTG 367
Qy 181 VFICVDVWFSIAEKNSYFDMINIVTQMRKORCGMIQTK 218
Db 368 VFICVDVWFSIAEKNSYFDMINIVTQMRKORCGMIQTK 405

RESULT 5
US-09-095-478-2
; Sequence 2, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUPT05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 463 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-09-095-478-2
```

	Query Match	100.0%;	Score 1174;	DB 10;	Length 463;	
	Best Local Similarity	100.0%;	Pred. No. 4.4e-119;			
	Matches 218;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 QNRDKRYRDLIPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ	60				
Db	225 QNRDKRYRDLIPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ	284				
QY	61 MVLNNCNVIAMTRIECGVIKCYSWPISLKEPFEHFSVLETFHVTQYFTVRVFG	120				
Db	285 MVLNNCNVIAMTRIECGVIKCYSWPISLKEPFEHFSVLETFHVTQYFTVRVFG	344				
QY	121 IVKSTGKSCQVXHLQFTKWPDHGTASADFFIKYVRYVRKSHITGPLLHVCBSAGVGRIG	180				
Db	345 IVKSTGKSCQVXHLQFTKWPDHGTASADFFIKYVRYVRKSHITGPLLHVCBSAGVGRIG	404				
QY	181 VFCVDVWVSAIEKNYSFDIMNIVTQMRKORCGMIQTK	218				
Db	405 VFCVDVWVSAIEKNYSFDIMNIVTQMRKORCGMIQTK	442				
RESULT 6						
US-10-311-764-4						
; Sequence 4, Application US/10311764						
; Publication No. US20040023245A1						
; GENERAL INFORMATION:						
; APPLICANT: INCYTE GENOMICS, INC.; AU-YOUNG, Janice K.						
; APPLICANT: BAUGHN, Mariah R.; DING, Li						
; APPLICANT: ELLIOTT, Vicki S.; GANDHI, Ameena R.						
; APPLICANT: GRIFFIN, Jennifer A.; HAFALIA, April J.A.						
; APPLICANT: KEARNEY, Liam; LEE, Ernestine A.						
; APPLICANT: LU, Yan; NGUYEN, Daniel B.						
; APPLICANT: ARVIZU, Chandra S.; RAMKUNAR, Jayalaxmi						
; APPLICANT: REDDY, Roopa M.; SANJANWALA, Madhusudan M.						
; APPLICANT: STEWART, Elizabeth A.; TANG, Y. Tom						
; APPLICANT: THORNTON, Michael B.; TRIBOULEY, Catherine M.						
; APPLICANT: CHAWLA, Narinder K.; YANG, Junning						
; APPLICANT: YAO, Monique G.; YUE, Henry						
; TITLE OF INVENTION: PROTEIN PHOSPHATASES						
; FILE REFERENCE: PI-0126 USN						
; CURRENT APPLICATION NUMBER: US/10/311,764						
; CURRENT FILING DATE: 2002-12-16						
; PRIOR APPLICATION NUMBER: PCT/US01/19442						
; PRIOR FILING DATE: 2001-06-14						
; PRIOR APPLICATION NUMBER: US 60/212,447						
; PRIOR FILING DATE: 2000-06-16						
; PRIOR APPLICATION NUMBER: US 60/213,746						
; PRIOR FILING DATE: 2000-06-22						
; PRIOR APPLICATION NUMBER: US 60/215,210						
; PRIOR FILING DATE: 2000-06-29						
; PRIOR APPLICATION NUMBER: US 60/216,529						
; PRIOR FILING DATE: 2000-07-06						
; PRIOR APPLICATION NUMBER: US 60/218,080						
; PRIOR FILING DATE: 2000-07-12						
; PRIOR APPLICATION NUMBER: US 60/220,117						
; PRIOR FILING DATE: 2000-07-21						
; NUMBER OF SEQ ID NOS: 18						
; SOFTWARE: PERL Program						
; SEQ ID NO 4						
; LENGTH: 420						
; TYPE: PRT						
; ORGANISM: Homo sapiens						
; FEATURE:						
; NAME/KEY: misc feature						
; OTHER INFORMATION: Incyte ID No. US20040023245A1 7476861CD1						
US-10-311-764-4						
Query Match	79.7%;	Score 936;	DB 15;	Length 420;		
Best Local Similarity	78.8%;	Pred. No. 3.6e-93;				
Matches 171;	Conservative 22;	Mismatches 24;	Indels 0;	Gaps 0;		
QY	2 NRDKNRYRDLIPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ	61				

Db	183 NREKNRYRDLIPYDSTRVPLGSKDYINASYIRIVNCGEYFYIATQGPLLSTIDDFWQ	242				
QY	62 VLENNCNVIAMTRIECGVIKCYSWPISLKEPFEHFSVLETFHVTQYFTVRVFOI	121				
Db	243 VLENNCNVIAMTRIEGGIIRKCYHYWPISLKKPLSLKHLRVLNQLQVFIIRMFQV	302				
QY	122 VKKSTGKSCQVXHLQFTKWPDHGTASADFFIKYVRYVRKSHITGPLLHVCBSAGVGRIG	181				
Db	303 VEKSTGTSUSVQLQFTKWPDHGTASADSFIKYIRYARKSHLTGPMVWVHCSAGIGRTG	362				
QY	182 FICVDVWVSAIEKNYSFDIMNIVTQMRKORCGMIQTK	218				
Db	363 FLCVDVWVSAIVNCNSFNIMDIVAQMRQSRGMVQTK	399				
RESULT 7						
US-09-095-478-4						
; Sequence 4, Application US/09095478						
; Publication No. US20030095970A1						
; GENERAL INFORMATION:						
; APPLICANT: Plowman, Gregory						
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE						
; TITLE OF INVENTION: PHOSPHATASE SUPTPOS AND						
; TITLE OF INVENTION: RELATED PRODUCTS AND						
; TITLE OF INVENTION: METHODS						
; NUMBER OF SEQUENCES: 25						
; CORRESPONDENCE ADDRESS:						
; ADDRESSEE: Lyon & Lyon						
; STREET: 633 West Fifth Street						
; CITY: Suite 4700						
; STATE: Los Angeles						
; COUNTRY: California						
; ZIP: 90071-2066						
; COMPUTER READABLE FORM:						
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb						
; MEDIUM TYPE: storage						
; COMPUTER: IBM Compatible						
; OPERATING SYSTEM: IBM P.C. DOS 5.0						
; SOFTWARE: FastSeq for Windows 2.0						
; CURRENT APPLICATION DATA:						
; APPLICATION NUMBER: US/09/095,478						
; FILING DATE:						
; CLASSIFICATION:						
; PRIOR APPLICATION DATA:						
; APPLICATION NUMBER:						
; FILING DATE:						
; ATTORNEY/AGENT INFORMATION:						
; NAME: Warburg, Richard J.						
; REGISTRATION NUMBER: 32,327						
; REFERENCE/DOCKET NUMBER: 224/115						
; TELECOMMUNICATION INFORMATION:						
; TELEPHONE: (213) 489-1600						
; TELEFAX: (213) 955-0440						
; TELEX: 67-3510						
; INFORMATION FOR SEQ ID NO: 4:						
; SEQUENCE CHARACTERISTICS:						
; LENGTH: 122 amino acids						
; TYPE: amino acid						
; STRANDEDNESS: single						
; TOPOLOGY: linear						
; MOLECULE TYPE: Peptide						
US-09-095-478-4						
Query Match	56.9%;	Score 668;	DB 10;	Length 122;		
Best Local Similarity	100.0%;	Pred. No. 1.3e-64;				
Matches 122;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
QY	57 DFWQWVLENNCNVIAMITREIECGVIKCYSWPISLKEPFEHFSVLETFHVTQYFTV	116				
Db	1 DFWQWVLENNCNVIAMITREIECGVIKCYSWPISLKEPFEHFSVLETFHVTQYFTV	60				

QY 117 RVFQIVKSTGKSCQVKHLQFTKWPDHGTPASADFFIKYRVYRKSHITGPELLVHCSAGV 176
|||
Db 61 RVFQIVKSTGKSCQVKHLQFTKWPDHGTPASADFFIKYRVYRKSHITGPELLVHCSAGV 120
|||
QY 177 GR 178
||
Db 121 GR 122

RESULT 8

US-09-095-478-5
; Sequence 5, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide

US-09-095-478-5
Query Match 48.2%; Score 566; DB 10; Length 122;
Best Local Similarity 83.6%; Pred. No. 1.7e-53;
Matches 102; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 57 DFQWMLNNCNVIAMITREIEGVIKCYSWPISLKEPPEFHSVFLETFHTVQYFTV 116
|||
Db 1 DFQWMLNNCNVIAMITREIEGVIKCYSWPISLKEPPEFHSVFLETFHTVQYFTV 60
|||
QY 117 RVFQIVKSTGKSCQVKHLQFTKWPDHGTPASADFFIKYRVYRKSHITGPELLVHCSAGV 176
|||
Db 61 RVFQIVKSTGKSHVQKHLQFTKWPDHGTPASADFFIKYRVYRKSHITGPELLVHCSAGV 120
|||
QY 177 GR 178
||
Db 121 GR 122

RESULT 9

US-09-095-478-7
; Sequence 7, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide

US-09-095-478-7
Query Match 46.9%; Score 550.5; DB 10; Length 381;
Best Local Similarity 49.5%; Pred. No. 3.7e-51;
Matches 110; Conservative 34; Mismatches 71; Indels 7; Gaps 3;

QY 1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASIRIVNHEEYFYIATQGLPETIEDFWQ 60
|||
Db 144 ENRRKNRYKNILFYDTRVPLGDEGGYINASIRIPVGTQEFYIATQGLPETIEDFWQ 203
|||
QY 61 MVLNNNCNVIAMITREIEGVIKCYSWPISLKEPPEFHSVFLETFHTVQYFTV 119
|||
Db 204 MWEQNSTVIAMWTQVEGEKIKCQRYWPSILGTTTMANERLALLRMQQLKGFIVRM 263
|||
QY 120 QIVKSTGKSCQVKHLQFTKWPDHGTPASADFFIKYRVYRKSHITGPELLVHCSAGV 176
|||
Db 264 ALEDIQTGEVRHSHLNFAMPDHPDTPSQDPLLTFTISYMRHRS--GPVITHCSAGI 320
|||
QY 177 GRGTGVPICVDVWFSAIEKNSYFDIMNIVTQMRKQRCGMIOTK 218
|||
Db 321 GRSGTLCIDVVLGLISQDLDFIDSLVRCMRILQRHGMVQTE 362
|||

RESULT 10

US-09-095-478-9

Sequence 9, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide

US-09-095-478-9

Query Match 46.1%; Score 541.5; DB 10; Length 358;
Best Local Similarity 47.0%; Pred. No. 3.2e-50;
Matches 103; Conservative 37; Mismatches 78; Indels 1; Gaps 1;
QY 1 QNRDKRYRDLDPVDSRVPLGKNKYINASYIRIVNHEEYFVIATQGPLPETIEDFWQ 60
Db 121 ENRRKNRYKNLLPYDATRVPLDGGYINASFIPVGEFFVYIACQGPLTTVGDFWQ 180
QY 61 MVLNENCNVAMITREIECGVIKCYSPISL-KEPLEFEHFSVLFETHVQVTVRVF 119
Db 181 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTMVSNRLRLALVRMQLKGFVVVRAM 240
QY 120 QIVKSTGKSCQVKHLOFTWPDHGTTPASADFFIKYVYVRKSHITGPTLVHCSAGVGR 179
Db 241 TLEDIQTRVHRHISHLNFTAWPDHDTSPQDDLLTFISYMRHHSRSGPIITHCSAGIGRS 300
QY 180 GVFTICVDVPSAIEKNYSFDMNIVTQMRKQRCGMIOTK 218
Db 301 GTLICIDVVLGLISQDLDFDISLVRMQLRQHGVMQTE 339

RESULT 11

US-10-060-065-35
Sequence 35, Application US/10060065
Publication No. US20030017480A1

GENERAL INFORMATION:

APPLICANT: Toshio Ota
APPLICANT: Takao Isogai
APPLICANT: Tetsuo Nishikawa
APPLICANT: Koji Hayashi
APPLICANT: Kaoru Otsuka
APPLICANT: Jun-ichi Yamamoto
APPLICANT: Shizuko Ishii
APPLICANT: Tomoyasu Sugiyama
APPLICANT: Ai Wakamatsu
APPLICANT: Keiichi Nagai
APPLICANT: Tetsuji Otsuki
APPLICANT: Shin-ichi Funahashi
APPLICANT: Chiaki Senoo
APPLICANT: Jun-ichi Nezu
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-099002 US/10/060,065
CURRENT APPLICATION NUMBER: PCT/JP00/05061
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: US 60/159,590
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: JP 11-248036
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 2000-241899
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
LENGTH: 1267
TYPE: PRT
ORGANISM: Homo sapiens
US-10-060-065-35

Query Match 46.1%; Score 541.5; DB 14; Length 1267;
Best Local Similarity 47.0%; Pred. No. 1.7e-49;
Matches 103; Conservative 37; Mismatches 78; Indels 1; Gaps 1;
QY 1 QNRDKRYRDLDPVDSRVPLGKNKYINASYIRIVNHEEYFVIATQGPLPETIEDFWQ 60
Db 1018 ENRRKNRYKNLLPYDATRVPLDGGYINASFIPVGEFFVYIACQGPLTTVGDFWQ 1077
QY 61 MVLNENCNVAMITREIECGVIKCYSPISL-KEPLEFEHFSVLFETHVQVTVRVF 119
Db 1078 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTMVSNRLRLALVRMQLKGFVVVRAM 1137
QY 120 QIVKSTGKSCQVKHLOFTWPDHGTTPASADFFIKYVYVRKSHITGPTLVHCSAGVGR 179
Db 1138 TLEDIQTRVHRHISHLNFTAWPDHDTSPQDDLLTFISYMRHHSRSGPIITHCSAGIGRS 1197
QY 180 GVFTICVDVPSAIEKNYSFDMNIVTQMRKQRCGMIOTK 218
Db 1198 GTLICIDVVLGLISQDLDFDISLVRMQLRQHGVMQTE 1236

RESULT 12

US-10-059-585-56
Sequence 56, Application US/10059585
Publication No. US20030082776A1
GENERAL INFORMATION:
APPLICANT: Ota, Toshio
APPLICANT: Isogai, Takao
APPLICANT: Nishikawa, Tetsuo
APPLICANT: Hayashi, Koji
APPLICANT: Otsuka, Kaoru
APPLICANT: Yamamoto, Jun-ichi

```
; APPLICANT: Iehii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-Ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-Ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; FILE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059,585
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 1267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-059-585-56

Query Match 46.1%; Score 541.5; DB 14; Length 1267;
Best Local Similarity 47.0%; Pred. No. 1.7e-49;
Matches 103; Conservative 37; Mismatches 78; Indels 1; Gaps 1;

QY 1 QNRDKNRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
Db 1018 ENRRKNRYKNILPYDAIRVPLGDEGGYINASFIKIPVGKEEFYVIACQGPLPTTVGDFWQ 1077
QY 61 MVLNNCNVIAMITREIECGVIKCYSWPISL-KEPFEFEHFSVFLTEHVTQYFTVRVF 119
Db 1078 MIWEQKSTVIAMWTQEVGEKIKQRYWPNILKTTMVSNNRLALVRMQLKGFVVRAM 1137
QY 120 QIVKSTGSKQCVKHLQFTKWPDHGTPASADFFIKYRVYRKSHITGPLLHVCSAGVGT 179
Db 1138 TLEDIQTRVVRHSHLNFTAWPDHPTSPQDDLLTFISYMRHHRSGPIITHCSAGIGRS 1197
QY 180 GFVICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOTK 218
Db 1198 GTLICIDVVLGLISQDLDFDISLVRMRLQRHGMVQTE 1236

RESULT 13
US-10-177-980-12
; Sequence 12, Application US/10177980
; Publication No. US20030166232A1
; GENERAL INFORMATION:
; APPLICANT: Saras, Jan
; APPLICANT: Franz, Petra
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Hellman, Ulf
; APPLICANT: Genez, Leonel Jorge
; APPLICANT: Heldin, Carl-Henrik
; TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
; FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/10/177,980
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/080,855
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 08/805,583
; PRIOR FILING DATE: 1997-02-25

; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 2466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-980-12

Query Match 46.1%; Score 541.5; DB 14; Length 2466;
Best Local Similarity 47.0%; Pred. No. 4e-49;
Matches 103; Conservative 37; Mismatches 78; Indels 1; Gaps 1;

QY 1 QNRDKNRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
Db 2217 ENRRKNRYKNILPYDAIRVPLGDEGGYINASFIKIPVGKEEFYVIACQGPLPTTVGDFWQ 2276
QY 61 MVLNNCNVIAMITREIECGVIKCYSWPISL-KEPFEFEHFSVFLTEHVTQYFTVRVF 119
Db 2277 MIWEQKSTVIAMWTQEVGEKIKQRYWPNILKTTMVSNNRLALVRMQLKGFVVRAM 2336
QY 120 QIVKSTGSKQCVKHLQFTKWPDHGTPASADFFIKYRVYRKSHITGPLLHVCSAGVGT 179
Db 2337 TLEDIQTRVVRHSHLNFTAWPDHPTSPQDDLLTFISYMRHHRSGPIITHCSAGIGRS 2396
QY 180 GFVICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOTK 218
Db 2397 GTLICIDVVLGLISQDLDFDISLVRMRLQRHGMVQTE 2435

RESULT 14
US-10-795-148-2
; Sequence 2, Application US/10795148
; Publication No. US20040224337A1
; GENERAL INFORMATION:
; APPLICANT: FOEHR, ERIK
; APPLICANT: JERECIC, JASNA
; APPLICANT: LORENTIC, GUSTAVO A.
; APPLICANT: URPER, ROMAN
; TITLE OF INVENTION: USE OF BIOMOLECULAR TARGETS IN THE
; FILE REFERENCE: AGYT-022
; CURRENT APPLICATION NUMBER: US/10/795,148
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/452,169
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2466
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-795-148-2

Query Match 46.1%; Score 541.5; DB 17; Length 2466;
Best Local Similarity 47.0%; Pred. No. 4e-49;
Matches 103; Conservative 37; Mismatches 78; Indels 1; Gaps 1;

QY 1 QNRDKNRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
Db 2217 ENRRKNRYKNILPYDAIRVPLGDEGGYINASFIKIPVGKEEFYVIACQGPLPTTVGDFWQ 2276
QY 61 MVLNNCNVIAMITREIECGVIKCYSWPISL-KEPFEFEHFSVFLTEHVTQYFTVRVF 119
Db 2277 MIWEQKSTVIAMWTQEVGEKIKQRYWPNILKTTMVSNNRLALVRMQLKGFVVRAM 2336
QY 120 QIVKSTGSKQCVKHLQFTKWPDHGTPASADFFIKYRVYRKSHITGPLLHVCSAGVGT 179
Db 2337 TLEDIQTRVVRHSHLNFTAWPDHPTSPQDDLLTFISYMRHHRSGPIITHCSAGIGRS 2396
QY 180 GFVICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOTK 218
Db 2397 GTLICIDVVLGLISQDLDFDISLVRMRLQRHGMVQTE 2435
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RESULT 15
US-09-802-669-46
; Sequence 46, Application US/09802669
; Patent No. US20020004490A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Ras Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/09/802,669
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 46
; LENGTH: 2485
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-669-46

Query Match 46.1%; Score 541.5; DB 9; Length 2485;
Best Local Similarity 47.0%; Pred. No. 4.1e-49;
Matches 103; Conservative 37; Mismatches 78; Indels 1; Gaps 1;

Qy 1 QNRDKNYRDILPYDSTRVPLGKNDYINASYIIVNHEEYFYIATCGPLPETIEDFWQ 60
Db 2236 ENRRKNRYKNILPYDATRVPLGDEGGYINASFIIKIPVKEFEFVVIACQGPLTTVGDFWQ 2295

Qy 61 MVLNNNCNVIAMITREIECGVIKCYWNPISL-KEPLEFEHFSVFELETFHVTOYFTVRVF 119
Db 2296 MIWEQSTVIAMTQVEVEGEKIKQRYWPNILGKTTWVSNELRLALVRMQQLKGFVVVRAM 2355

Qy 120 QIVKKSTGKSCVKHLOFTKWPDHGTTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGR 179
Db 2356 TLEDIQTRVVRHISHLNFTAWPDHDTSPQDDLLTFISYMRHHRSGFIITHCSAGIGRS 2415

Qy 180 GVFLCVDVVFSAIEKNYSFDMNIVTQMRKORCGMIQTK 218
Db 2416 GTLICIDVVLGLISQDLDFDISDLVRCNRLQRHGAWQTE 2454

Search completed: December 1, 2004, 12:52:39
Job time : 398.117 secs

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OM protein - protein search, using sw model

Run on: December 1, 2004, 12:07:42 ; Search time 23.5848 Seconds
(without alignments)
612.993 Million cell updates/sec

Title: US-09-095-478A-7_COPY_188_405

Perfect score: 1174

Sequence: 1 QNRDKRYRDLFYDSTRV.....DIMNIVTQMKQRCGMIIQK 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541.5	46.1	2465	2	US-08-596-291-3
2	541.5	46.1	2465	3	US-09-100-804-3
3	541.5	46.1	2466	3	US-09-080-855-12
4	541.5	46.1	2466	4	US-09-566-076-12
5	541.5	46.1	2466	5	PCT-US94-09943-2
6	541.5	46.1	2485	3	US-09-290-640-46
7	541.5	46.1	2485	4	US-09-665-615B-46
8	467	39.8	913	1	US-09-848-294-2
9	462.5	39.4	278	1	US-08-201-697-16
10	462	39.4	231	2	US-08-446-345-37
11	462	39.4	244	4	US-09-848-294-7
12	456	38.8	242	2	US-08-585-992-21
13	456	38.8	242	2	US-09-144-925-21
14	444	37.8	1337	3	US-08-584-585-2
15	444	37.8	1337	4	US-09-447-533-2
16	444	37.8	1337	5	PCT-US95-05512-2
17	439.5	37.4	232	2	US-08-446-345-38
18	434	37.0	296	4	US-10-374-539-2
19	434	37.0	1457	2	US-08-552-971-3
20	434	37.0	1457	2	US-08-449-644-1
21	434	37.0	1457	2	US-08-087-244A-1
22	434	37.0	1457	2	US-08-991-258A-3
23	434	37.0	1457	2	US-08-769-399-3
24	434	37.0	1457	3	US-08-991-953A-3
25	432.5	36.8	1911	1	US-08-348-006B-5
26	432.5	36.8	1911	2	US-08-800-825A-5
27	432.5	36.8	1911	3	US-09-158-657-5

28 432.5 36.8 1911 5 PCT-US94-10166-5 Sequence 5, Appli
29 432 36.8 246 4 US-09-848-294-9 Sequence 9, Appli
30 431.5 36.8 254 2 US-08-685-992-14 Sequence 14, Appli
31 431.5 36.8 254 2 US-09-144-925-14 Sequence 14, Appli
32 431 36.7 1188 1 US-08-201-697-4 Sequence 4, Appli
33 428 36.5 1439 2 US-08-449-644-2 Sequence 2, Appli
34 428 36.5 1439 2 US-08-087-244A-2 Sequence 2, Appli
35 427.5 36.4 1501 2 US-08-447-464-3 Sequence 3, Appli
36 427.5 36.4 1501 2 US-08-716-679-3 Sequence 3, Appli
37 427 36.4 1187 1 US-08-201-697-2 Sequence 2, Appli
38 424 36.1 253 2 US-08-685-992-11 Sequence 11, Appli
39 424 36.1 253 2 US-09-144-925-11 Sequence 11, Appli
40 423 36.0 1452 2 US-08-449-644-8 Sequence 8, Appli
41 423 36.0 1452 2 US-08-087-244A-8 Sequence 36, Appli
42 422.5 36.0 1174 2 US-08-446-345-36 Sequence 4, Appli
43 422 35.9 1452 2 US-08-652-971-4 Sequence 4, Appli
44 422 35.9 1452 2 US-08-991-258A-4 Sequence 4, Appli
45 422 35.9 1452 2 US-08-769-399-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-596-291-3
; Sequence 3, Application US/08596291
; Patent No. 5821075
; GENERAL INFORMATION:
; APPLICANT: GONEZ, LEONEL JORGE
; APPLICANT: SARAS, JAN
; APPLICANT: CLAESSON-WELSH, LENA
; APPLICANT: HELDIN, CARL-HENRIK
; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLFF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/596,291
; FILING DATE: 09-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/115,573
; FILING DATE: 01-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REFERENCE NUMBER: 31,616
; REGISTRATION/DOCKET NUMBER: LO461/7000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; TELEX: 92-1742 EZEKIEL
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2465 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-596-291-3

Query Match 46.1%; Score 541.5; DB 2; Length 2465;
Best Local Similarity 47.0%; Pred. No. 3.4e-53;

Best Local Similarity 47.0%; Pred. No. 3.4e-53;
Matches 103; Conservative 37; Mismatches 78; Indels 1; Gaps 1;
QY 1 QNRDKNRVDRILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATOGPLPETIEDFWQ 60
Db 2216 ENRRKNRYKNILPYDATRVPLDGGYINAFIKIPVGEFFYIACQGPLTTVGDFWQ 2275
QY 61 MVLNNNCNVIAMITREIECGVIKCYSWPISL-KEPFEFEHFSVLETHVTHVQYFTVRVF 119
Db 2276 MIWEQKSTVIAMTQVEGEKIKCQRYWPNILGKTTMVSNNRLRLALVRMQQLKGFVVVRAM 2335
QY 120 QIVKSTGSKQCVKHLQFTKWPDPHGTPASADFFIKYVRYVRKSHITGPLLHVCASAGVGT 179
Db 2336 TLEDIQTRVRIHSHLNTAWPDHDTSPQDDLLTFISYMRHHSRGPITTHCSAGIGRS 2395
QY 180 GVFIQVDVVVFAIEKNYSFDIMNIVTQMRKQRCGMIOQTK 218
Db 2396 GTLICIDVVVLGLISQDLDFDISDLVRCMLQRHGMVQTE 2434

RESULT 3

US-09-080-855-12
; Sequence 12, Application US/09080855A
; Patent No. 6083721
; GENERAL INFORMATION:
; APPLICANT: Saraz, Jan
; APPLICANT: Franz, Petra
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Hellman, Ulf
; APPLICANT: Genez, Leonel Jorge
; APPLICANT: Heldin, Carl-Henrik
; TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
; FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/09/080,855A
; CURRENT FILING DATE: 1998-05-18
; EARLIER APPLICATION NUMBER: 08/805,583
; EARLIER FILING DATE: 1997-02-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 2466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-080-855-12

Query Match 46.1%; Score 541.5; DB 3; Length 2466;
Best Local Similarity 47.0%; Pred. No. 3.4e-53;
Matches 103; Conservative 37; Mismatches 78; Indels 1; Gaps 1;

QY 1 QNRDKNRVDRILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATOGPLPETIEDFWQ 60
Db 2217 ENRRKNRYKNILPYDATRVPLDGGYINAFIKIPVGEFFYIACQGPLTTVGDFWQ 2276
QY 61 MVLNNNCNVIAMITREIECGVIKCYSWPISL-KEPFEFEHFSVLETHVTHVQYFTVRVF 119
Db 2277 MIWEQKSTVIAMTQVEGEKIKCQRYWPNILGKTTMVSNNRLRLALVRMQQLKGFVVVRAM 2336
QY 120 QIVKSTGSKQCVKHLQFTKWPDPHGTPASADFFIKYVRYVRKSHITGPLLHVCASAGVGT 179
Db 2337 TLEDIQTRVRIHSHLNTAWPDHDTSPQDDLLTFISYMRHHSRGPITTHCSAGIGRS 2396
QY 180 GVFIQVDVVVFAIEKNYSFDIMNIVTQMRKQRCGMIOQTK 218
Db 2397 GTLICIDVVVLGLISQDLDFDISDLVRCMLQRHGMVQTE 2435

RESULT 4

US-09-566-076-12
; Sequence 12, Application US/09566076
; Patent No. 6475775
; GENERAL INFORMATION:
; APPLICANT: Saraz, Jan
; APPLICANT: Franz, Petra

Matches 103; Conservative 37; Mismatches 78; Indels 1; Gaps 1;
QY 1 QNRDKNRVDRILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATOGPLPETIEDFWQ 60
Db 2216 ENRRKNRYKNILPYDATRVPLDGGYINAFIKIPVGEFFYIACQGPLTTVGDFWQ 2275
QY 61 MVLNNNCNVIAMITREIECGVIKCYSWPISL-KEPFEFEHFSVLETHVTHVQYFTVRVF 119
Db 2276 MIWEQKSTVIAMTQVEGEKIKCQRYWPNILGKTTMVSNNRLRLALVRMQQLKGFVVVRAM 2335
QY 120 QIVKSTGSKQCVKHLQFTKWPDPHGTPASADFFIKYVRYVRKSHITGPLLHVCASAGVGT 179
Db 2336 TLEDIQTRVRIHSHLNTAWPDHDTSPQDDLLTFISYMRHHSRGPITTHCSAGIGRS 2395
QY 180 GVFIQVDVVVFAIEKNYSFDIMNIVTQMRKQRCGMIOQTK 218
Db 2396 GTLICIDVVVLGLISQDLDFDISDLVRCMLQRHGMVQTE 2434

RESULT 2

US-100-804-3
; Sequence 3, Application US/09100804
; Patent No. 6066472
; GENERAL INFORMATION:
; APPLICANT: GONEZ, LEONEL JORGE
; APPLICANT: SARAS, JAN
; APPLICANT: CLAESON-WELSH, LENA
; APPLICANT: HELDIN, CARL-HENRIK
; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,804
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/596,291
; FILING DATE: 09-AUG-1996
; APPLICATION NUMBER: US 08/115,573
; FILING DATE: 01-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09943
; FILING DATE: 01-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: L0461/7003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2465 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-100-804-3
Query Match 46.1%; Score 541.5; DB 3; Length 2465;

```
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Hellman, Ulf
; APPLICANT: Gomez, Leonel Jorge
; APPLICANT: Heidin, Carl-Henrik
; TITLE OF INVENTION: PARC, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTEP1
; FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/09/566,076
; CURRENT FILING DATE:
; EARLIER APPLICATION NUMBER: 09/080,855
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 2466
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US94-09943-2
; US-09-566-076-12

Query Match          46.1%; Score 541.5; DB 4; Length 2466;
Best Local Similarity 47.0%; Pred. No. 3.4e-53;
Matches 103; Conservative 37; Mismatches 78; Indels 1; Gaps 1;

QY 1 QNRDKNRYRDIILPYDSTRVPLGKKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
Db 2217 ENRRKNRYKNILPYDATRVPLGDEGGYINASFIPKIPVGKEEFVYIACQGPLPTTVGDFWQ 2276
QY 61 MVLNNCNVIAITREIECGVIKCYWPISL-KEPLEFEHFSVPLETHVTOYFTVRVF 119
Db 2277 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTMVSNNRLALVRMQQLKGFVVRAM 2336
QY 120 QIVKXSTGKSQCVKHLQFTKPDHGTTPASADFFIKYRVYVRKSHITGPLLHVCAGVGR 179
Db 2337 TLEDIQTREVRHISHLNFTAWPDHPTSPQDLDLTFISYMRHHRSGPIITHCSAGIGRS 2396
QY 180 GVFCVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOTK 218
Db 2397 GTLICIDVVLGLISQDLDFISDLVRCMLQRHGMVQTE 2435

RESULT 5
PCT-US94-09943-2
; Sequence 2, Application PC/TUS9409943
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09943
; FILING DATE: 01-SEP-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/115,573
; FILING DATE: 01-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: TWOMEY, MICHAEL J.
; REGISTRATION NUMBER: P-38,349
; REFERENCE/DOCKET NUMBER: L0461/7000WO
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; TELEX: 92-1742 EZEKIEL
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2466 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-09943-2

Query Match          46.1%; Score 541.5; DB 5; Length 2466;
Best Local Similarity 47.0%; Pred. No. 3.4e-53;
Matches 103; Conservative 37; Mismatches 78; Indels 1; Gaps 1;

QY 1 QNRDKNRYRDIILPYDSTRVPLGKKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
Db 2217 ENRRKNRYKNILPYDATRVPLGDEGGYINASFIPKIPVGKEEFVYIACQGPLPTTVGDFWQ 2276
QY 61 MVLNNCNVIAITREIECGVIKCYWPISL-KEPLEFEHFSVPLETHVTOYFTVRVF 119
Db 2277 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTMVSNNRLALVRMQQLKGFVVRAM 2336
QY 120 QIVKXSTGKSQCVKHLQFTKPDHGTTPASADFFIKYRVYVRKSHITGPLLHVCAGVGR 179
Db 2337 TLEDIQTREVRHISHLNFTAWPDHPTSPQDLDLTFISYMRHHRSGPIITHCSAGIGRS 2396
QY 180 GVFCVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOTK 218
Db 2397 GTLICIDVVLGLISQDLDFISDLVRCMLQRHGMVQTE 2435

RESULT 6
US-09-290-640-46
; Sequence 46, Application US/09290640
; Patent No. 6204055
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0351
; CURRENT APPLICATION NUMBER: US/09/290,640
; CURRENT FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 2485
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-290-640-46

Query Match          46.1%; Score 541.5; DB 3; Length 2485;
Best Local Similarity 47.0%; Pred. No. 3.4e-53;
Matches 103; Conservative 37; Mismatches 78; Indels 1; Gaps 1;

QY 1 QNRDKNRYRDIILPYDSTRVPLGKKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
Db 2236 ENRRKNRYKNILPYDATRVPLGDEGGYINASFIPKIPVGKEEFVYIACQGPLPTTVGDFWQ 2295
QY 61 MVLNNCNVIAITREIECGVIKCYWPISL-KEPLEFEHFSVPLETHVTOYFTVRVF 119
Db 2296 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTMVSNNRLALVRMQQLKGFVVRAM 2355
QY 120 QIVKXSTGKSQCVKHLQFTKPDHGTTPASADFFIKYRVYVRKSHITGPLLHVCAGVGR 179
Db 2356 TLEDIQTREVRHISHLNFTAWPDHPTSPQDLDLTFISYMRHHRSGPIITHCSAGIGRS 2415
QY 180 GVFCVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOTK 218
Db 2416 GTLICIDVVLGLISQDLDFISDLVRCMLQRHGMVQTE 2454
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RESULT 7
US-09-665-615B-46
; Sequence 46, Application US/09665615B
; Patent No. 6653133
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0502
; CURRENT APPLICATION NUMBER: US/09/665,615B
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/230,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 46
; LENGTH: 2485
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo
US-09-665-615B-46

Query Match 46.1%; Score 541.5; DB 4; Length 2485;
Best Local Similarity 47.0%; Pred. No. 3.4e-53;
Matches 103; Conservative 37; Mismatches 78; Indels 1; Gaps 1;

QY 1 QNRDKNRYRDLIPYDSTRVPLGKKNKOVINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2236 ENRRKNRYKILPYDATRVPLGDEGGYINAFIKIPVKEEFYIACQGPLPTTVGDFWQ 2295

QY 61 MVLNNCNVIAITREIECGVIKCYSWPISL-KEPFEHFSVLETFHVTVYFTVRVF 119
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2296 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTVSNRLRLVRCMLQKGFVVRAM 2355

QY 120 QIVKSKSGQCVKHQFTKWPDRHTPASADFFIKYVRYVKSHITGPLEVHCSAGVGR 179
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2356 TLEDIQTRVYRHSHLNTAHPDHTPSQPDLLTFISYMRHHSRSPITTHCSAGIGRS 2415

QY 180 GVFCVDVVSFAEKNSYFDIMNIVTOMRKORCMIOTK 218
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2416 GTLICIDWLGSLSQDLDFDISDLVRCMLQRHGMVQTE 2454

RESULT 8
US-09-848-294-2
; Sequence 2, Application US/09848294
; Patent No. 6479640
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el
; TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal
; TITLE OF INVENTION: Adhesions and Uses Therefor
; FILE REFERENCE: CSHL90-04FZA
; CURRENT APPLICATION NUMBER: US/09/848,294
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 09/235,251
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 08/759,536
; PRIOR FILING DATE: 1996-12-04
; PRIOR APPLICATION NUMBER: 08/107,420
; PRIOR FILING DATE: 1993-08-16
; PRIOR APPLICATION NUMBER: 07/663,579
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 07/494,036
; PRIOR FILING DATE: 1990-03-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 913
; TYPE: PRT
; ORGANISM: Homosapiens
US-09-848-294-2
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Query Match 39.8%; Score 467; DB 4; Length 913;
Best Local Similarity 42.3%; Pred. No. 3.7e-45;
Matches 96; Conservative 35; Mismatches 78; Indels 18; Gaps 5;

QY 1 QNRDKNRYRDLIPYDSTRVPLGKKNKDYINASYI-----RIVNHEEYFYIATQGPLPE 53
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 669 QNLDKNRYKDLVYDTRVLQGNEDYINASYVNMIEIPAANLVNK-----YIATQGPLPH 723

QY 54 TIEDFWQVLENNCNVIAITREIECGVIKCYSWPISLKEPFEH--FSVFLETFHVT 111
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 724 TCAQFQCVVVDQKLSLVMLTTLTERGRYKCHQYWP---DPPDVNHHGGFHICQSEDCT 780

QY 112 QYFTVRVFIQVKSTGKSCVXHLQFTKWPDRHTPASADFFIKYVRYVKSHI-TGPLLV 170
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 781 IAYVSREMLVTNTQTGEEHTVTHLQYVAVPDRHGIPDDSDDFLEFVNYVRSRLRVDSFVLV 840

QY 171 HCSAGVGRGVFCVDVVSFAEKNSYFDIMNIVTOMRKORCMIOQT 217
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 841 HCSAGIGRTGVLVTMETAMCLTERNLPIYPLDLIVRCMLQRHGMVQOT 887

RESULT 9
US-08-201-697-16
; Sequence 16, Application US/08201697
; Patent No. 5705623
; GENERAL INFORMATION:
; APPLICANT: Wiggins, Roger C.
; APPLICANT: Thomas, Peedikavil E.
; TITLE OF INVENTION: Mammalian Glomerular Epithelial Protein
; TITLE OF INVENTION: 1
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/201,697
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UM 9783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 278 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-201-697-16

Query Match 39.4%; Score 462.5; DB 1; Length 278;
Best Local Similarity 43.0%; Pred. No. 2.3e-45;
Matches 98; Conservative 38; Mismatches 79; Indels 13; Gaps 5;

QY 1 QNRDKNRYRDLIPYDSTRVPLGK-----NKDYINASYIRIVNHEEYFYIATQGPLPETI 55
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 45 ENRGKNRYNIIIPYDATRVKLSNVDDPCSDYINASIPGNFRRE--YIVTQGPLGPKTK 102

QY 56 EDFWQVLENNCNVIAITREIECGVIKCYSWPISLKEPFEHFSVLETFHVTVYFT 115
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 103 DDFWQVLENNCNVIAITREIECGVIKCYSWPISLKEPFEHFSVLETFHVTVYFT 161
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QY 116 VRVFTQV-KKSTCKSCQVKKHLOFTKPDHGTASADFFIKYVR-----YVRKSHITGPLL 170
Db 162 IREFKTCGEBQDAHLRIHFHYVWPDHGVPETTSQSLQFVTRVDYINRSPGPTV 221
QY 171 HCSAGVGRGTGVTFCVDVWFSAEIKNYSFDMINIVTQMRKORCGMIQT 218
Db 222 HCSAGVGRGTGVTFCVDVWFSAEIKNYSFDMINIVTQMRKORCGMIQT 269
RESULT 10
US-08-446-345-37
; Sequence 37, Application US/08446345
; Patent No. 5831009
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Moller, Niels P.H.
; APPLICANT: Moller, Karin B.
; TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE
; TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE
; TITLE OF INVENTION: PHOSPHATASES PTP-D1
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: N.Y.
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,345
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/234,440
; FILING DATE: 28-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30742
; REFERENCE/DOCKET NUMBER: 7683-054
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212) 869-8864
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-446-345-37

Query Match 39.4%; Score 462; DB 2; Length 231;
Best Local Similarity 42.0%; Pred. No. 2.1e-45;
Matches 95; Conservative 35; Mismatches 78; Indels 18; Gaps 5;
QY 2 NRDKRYRDLIPYDSTRVPLGKKNKYINASYI-----RIVNHEEYFYIATQGLPET 54
Db 1 NLDKNRYKDVLPYDTRVLVLLQGNEDYINASYVNMETPAANLVNK-----YIATQGLPET 55
QY 55 IEDFWQVLENNCNVIAITREIECGVICKYSWPISLKEPLFEH--FSVFLETFHTQ 112
Db 56 CAQFQVQVWQKLSLIVMLTTLTERGRTKCHQWP---DPPVMNHGGFHIQCSSEDCI 112
QY 113 YFTVRVFIQVKSTGKSCQVKKHLOFTKPDHGTASADFFIKYVRKSHI-TGPLL 171
Db 113 AVYSREMLVTNTQTGEHTVTHLQYVAVPDHGIPODSSDFLEFVNVYVRSRLVDSPEVLVH 172
QY 172 CSAGVGRGTGVTFCVDVWFSAEIKNYSFDMINIVTQMRKORCGMIQT 217
Db 173 CSAGVGRGTGVTFCVDVWFSAEIKNYSFDMINIVTQMRKORCGMIQT 218

Db 173 CSAGVGRGTGVTFCVDVWFSAEIKNYSFDMINIVTQMRKORCGMIQT 218
RESULT 11
US-09-848-294-7
; Sequence 7, Application US/09848294
; Patent No. 6479640
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el
; TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal
; TITLE OF INVENTION: Adhesions and Uses Therefor
; FILE REFERENCE: CSHL90-04PZA
; CURRENT APPLICATION NUMBER: US/09/848,294
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 09/235,251
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 08/759,536
; PRIOR FILING DATE: 1996-12-04
; PRIOR APPLICATION NUMBER: 08/107,420
; PRIOR FILING DATE: 1993-08-16
; PRIOR APPLICATION NUMBER: 07/663,579
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 07/494,036
; PRIOR FILING DATE: 1990-03-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homosapiens
; US-09-848-294-7

Query Match 39.4%; Score 462; DB 4; Length 244;
Best Local Similarity 42.0%; Pred. No. 2.2e-45;
Matches 95; Conservative 35; Mismatches 78; Indels 18; Gaps 5;
QY 2 NRDKRYRDLIPYDSTRVPLGKKNKYINASYI-----RIVNHEEYFYIATQGLPET 54
Db 1 NLDKNRYKDVLPYDTRVLVLLQGNEDYINASYVNMETPAANLVNK-----YIATQGLPET 55
QY 55 IEDFWQVLENNCNVIAITREIECGVICKYSWPISLKEPLFEH--FSVFLETFHTQ 112
Db 56 CAQFQVQVWQKLSLIVMLTTLTERGRTKCHQWP---DPPVMNHGGFHIQCSSEDCI 112
QY 113 YFTVRVFIQVKSTGKSCQVKKHLOFTKPDHGTASADFFIKYVRKSHI-TGPLL 171
Db 113 AVYSREMLVTNTQTGEHTVTHLQYVAVPDHGIPODSSDFLEFVNVYVRSRLVDSPEVLVH 172
QY 172 CSAGVGRGTGVTFCVDVWFSAEIKNYSFDMINIVTQMRKORCGMIQT 217
Db 173 CSAGVGRGTGVTFCVDVWFSAEIKNYSFDMINIVTQMRKORCGMIQT 218

RESULT 12
US-08-685-992-21
; Sequence 21, Application US/08685992
; Patent No. 5912138
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas
; APPLICANT: Flint, Andrew J.
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,992
FILING DATE: 25-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-03
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-685-992-21

Query Match 38.8%; Score 456; DB 2; Length 242;
Best Local Similarity 41.7%; Pred. No. 1.1e-44;
Matches 96; Conservative 35; Mismatches 73; Indels 26; Gaps 7;

QY 1 QNRDKRYRDLIPYDSTRVPLGKNKDYINASYI-----RIVNHEEYFYIATQGLPE 53
DB 11 QNLDKRYKDVLPYDTRVLQGNEDYINASYNMEIPAANLYNK-----YIATQGLPH 65
QY 54 TIEDFMQWLENNCNVIAITREIECGVTKCYSWPISLKEPFEHFSVLETFHV--- 110
DB 66 TCAQFQVQWVDQKLSLVMLTLTLTERGRTKCHQWP---DPPDMNHGG-----FHIQCQ 117
QY 111 TQVFTVRVFO--IVKSTGKSCQVKHLQFTKPDHGTTPASADFFIKYVRVVRKSHI--TGP 167
DB 118 SEDCTIAYVSMVNTQTGSEHTVTHLQYVAMPDHGIPDDSDSDFLEFVNVYVRSVRDSEP 177
QY 168 LLVHCSAGVGRGTGVFCVDVFSIAEKNSYFDMNIVTQMRKORCGMIQT 217
DB 178 VLVHCSAGIGRTGVLVMTMETAMCLTERNLPIYPLDIVRKMRDQAMMVQT 227

RESULT 13
US-09-144-925-21
Sequence 21, Application US/09144925
Patent No. 5951979
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02421-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,925

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,992
FILING DATE: July 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-03Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-144-925-21

Query Match 38.8%; Score 456; DB 2; Length 242;
Best Local Similarity 41.7%; Pred. No. 1.1e-44;
Matches 96; Conservative 35; Mismatches 73; Indels 26; Gaps 7;

QY 1 QNRDKRYRDLIPYDSTRVPLGKNKDYINASYI-----RIVNHEEYFYIATQGLPE 53
DB 11 QNLDKRYKDVLPYDTRVLQGNEDYINASYNMEIPAANLYNK-----YIATQGLPH 65
QY 54 TIEDFMQWLENNCNVIAITREIECGVTKCYSWPISLKEPFEHFSVLETFHV--- 110
DB 66 TCAQFQVQWVDQKLSLVMLTLTLTERGRTKCHQWP---DPPDMNHGG-----FHIQCQ 117
QY 111 TQVFTVRVFO--IVKSTGKSCQVKHLQFTKPDHGTTPASADFFIKYVRVVRKSHI--TGP 167
DB 118 SEDCTIAYVSMVNTQTGSEHTVTHLQYVAMPDHGIPDDSDSDFLEFVNVYVRSVRDSEP 177
QY 168 LLVHCSAGVGRGTGVFCVDVFSIAEKNSYFDMNIVTQMRKORCGMIQT 217
DB 178 VLVHCSAGIGRTGVLVMTMETAMCLTERNLPIYPLDIVRKMRDQAMMVQT 227

RESULT 14
US-08-854-585-2
Sequence 2, Application US/08854585
Patent No. 6114140
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas K. and stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine Phosphatase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, Suite 6300
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,585
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/237,940
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27866/31954

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1337 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-854-585-2

Query Match 37.8%; Score 444; DB 3; Length 1337;
Best Local Similarity 41.2%; Pred. No. 3e-42;
Matches 93; Conservative 42; Mismatches 79; Indels 12; Gaps 5;
QY 1 QNRDKNRYRDLIPYDSTRVPLG-----KNKDYINASYIRIVNHEEYFYIATQGLPETIE 56
DB 1064 ENRGKRNRYNVLPIYDISRVKLSVQTHSTDDYINANYMPGVHKKD--FIATQGLPLPNTLK 1121
QY 57 DFQWMLNENNCNVIAMITREICGVKICYSYWPISLKEPFEHFSVLETFHVTQYFTV 116
DB 1122 DFRWVWKNVYALIMLTCKVEQRTKCEYWP--SKQAQDYGDITVAMTSEIVLPWTI 1179
QY 117 RVFQIVKKSTGKSCVKKHLOFTKWDHGTDPASADFFIKY---VR-YVRKSHITGPLLIVHC 172
DB 1180 RDTVKNIQTSSEHPLRQFHFTSWPDHGVEDTDLINFRYLVRDYNKQSPSPILVHC 1239
QY 173 SAGVGRGTGVFICVDVVSFAIEKNYSFDIMNIVTQMRKQRCGMIOQTK 218
DB 1240 SAGVGRGTGTFIADRLIYQIENENTVDVYGVYDLRMRHPLMVQTE 1285

RESULT 15
US-09-447-533-2
Sequence 2, Application US/09447533
Patent No. 6552169
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas K.
Ostman, Arne
TITLE OF INVENTION: DENSITY ENHANCED PROTEIN TYROSINE
PHOSPHATASES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group PLLC
STREET: Suite 6300, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 980104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/447,533
FILING DATE: 23-No. 6552169-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Rosenman Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 200125.402C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1337 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-447-533-2

Query Match 37.8%; Score 444; DB 4; Length 1337;
Best Local Similarity 41.2%; Pred. No. 3e-42;
Matches 93; Conservative 42; Mismatches 79; Indels 12; Gaps 5;
QY 1 QNRDKNRYRDLIPYDSTRVPLG-----KNKDYINASYIRIVNHEEYFYIATQGLPETIE 56
DB 1064 ENRGKRNRYNVLPIYDISRVKLSVQTHSTDDYINANYMPGVHKKD--FIATQGLPLPNTLK 1121
QY 57 DFQWMLNENNCNVIAMITREICGVKICYSYWPISLKEPFEHFSVLETFHVTQYFTV 116
DB 1122 DFRWVWKNVYALIMLTCKVEQRTKCEYWP--SKQAQDYGDITVAMTSEIVLPWTI 1179
QY 117 RVFQIVKKSTGKSCVKKHLOFTKWDHGTDPASADFFIKY---VR-YVRKSHITGPLLIVHC 172
DB 1180 RDTVKNIQTSSEHPLRQFHFTSWPDHGVEDTDLINFRYLVRDYNKQSPSPILVHC 1239
QY 173 SAGVGRGTGVFICVDVVSFAIEKNYSFDIMNIVTQMRKQRCGMIOQTK 218
DB 1240 SAGVGRGTGTFIADRLIYQIENENTVDVYGVYDLRMRHPLMVQTE 1285

Search completed: December 1, 2004, 12:18:55
Job time : 24.5848 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 1, 2004, 12:07:39 ; Search time 76.4912 Seconds
(without alignments)
1022.379 Million cell updates/sec

Title: US-09-095-478A-7_COPY_188_405
Perfect score: 1174
Sequence: 1 QNRDKNRYRDLPLDYSTRVP.....DIMNIVTQMRKQRCGMIQTK 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:.*
1: Geneseq1980s:.*
2: Geneseq1990s:.*
3: Geneseq2000s:.*
4: Geneseq2001s:.*
5: Geneseq2002s:.*
6: Geneseq2003as:.*
7: Geneseq2003bs:.*
8: Geneseq2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1174	100.0	405	2 AAW89251	Aw89251 Mouse PTP
2	1174	100.0	426	2 AAW89249	Aw89249 Mouse PTP
3	1174	100.0	463	2 AAW89250	Aw89250 Mouse PTP
4	936	79.7	261	6 AAE37994	Aae37994 Human kin
5	936	79.7	412	6 AAE37996	Aae37996 Human kin
6	936	79.7	420	5 AAE14454	Aae14454 Human kin
7	928	79.0	398	5 AAG30845	Abg30845 Human tyr
8	928	79.0	398	7 ADD89795	Add89795 Human tyr
9	928	79.0	409	7 ADE09123	Ade09123 Novel pro
10	928	79.0	508	7 ADE08106	Ade08106 Novel pro
11	928	79.0	561	4 AAG06042	Abg06042 Novel hum
12	572	48.2	348	8 ADK71863	Adk71863 Human kin
13	566	48.2	122	2 AAW89252	Aw89252 Rat PTP10
14	541.5	46.1	766	6 ABU70688	Abu70688 Human adi
15	541.5	46.1	1267	4 AAG67637	Aag67637 Amino aci
16	541.5	46.1	1287	4 AAG67458	Aag67458 Amino aci
17	541.5	46.1	2466	2 AAR71498	Aar71498 Human pro
18	541.5	46.1	2466	2 AAW75999	Aaw75999 Intracell
19	541.5	46.1	2466	3 AAY90272	Aay90272 Human PTP
20	541.5	46.1	2485	3 AAB19343	Aab19343 Amino aci
21	541.5	46.1	2485	7 ADJ69543	Adj69543 Human hea
22	541.5	46.1	2485	8 ADL27685	Adl27685 Human Fas
23	541.5	46.1	2485	8 ADM53457	Adm53457 Human Fas
24	499	42.5	235	5 ADI17283	Adi17283 Polypteti
25	482	41.1	1028	8 ADF43232	Adf43232 Mouse PTP

ALIGNMENTS

RESULT 1
AAW89251
ID AAW89251 standard; protein; 405 AA.
XX
AC AAW89251;
XX

DT 10-MAR-1999 (first entry)
XX
XX Mouse PTP05 isoform #2.
DE

XX
XX PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;
KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;
KW neurodegenerative disease; neuronal survival; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease.
XX
Mus sp.
XX
WO9849317-A2.
XX
05-NOV-1998.
XX
27-APR-1998; 98WO-US008439.
XX

PR 28-APR-1997; 97US-0044428P.
PR 20-MAY-1997; 97US-0047222P.
PR 11-JUN-1997; 97US-0049477P.
PR 11-JUN-1997; 97US-0049756P.
PR 18-JUN-1997; 97US-0049914P.
PR 23-OCT-1997; 97US-0063595P.
XX
PA (SUG-) SUGEN INC.
XX
XX Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;
PI Courtneidge SA, App H, Hui TH;
XX N-PSDB; AAW81746.
XX
XX New nucleic acid encoding specific protein tyrosine phosphatases - useful
PT for identifying specific modulators for treatment and prevention of
PT cancer and neurodegenerative disease.
XX
PS Claim 2; Page 158-160; 193pp; English.
XX
XX The present invention describes isolated, enriched or purified nucleic
CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The
CC present sequence represents mouse PTP05. The above proteins, other than
CC ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify

Ado55173 Protein #
Adl16191 Human pro
Adf43234 Human PTP
Aaw12522 Protein t
Aay25156 Human PTP
Aag79333 PTPH1. 8/
Ad22982 Human pro
Adl16189 Human pro
Adf43230 Human PTP
Aag78282 Human PTP
Aao24268 Murine va
Aab53384 Human pro
Aab19773 Mouse vas
Ado04584 Human HPT
Ado04585 Human HPT
Ado04582 Human HPT
Abr57182 Human PTP
Aab19774 Human pro
Aam78821 Human pro
Aae20278 Human lun

CC substances that modulate their activity (i.e. agonists and antagonists,
 CC including NBP) in vivo or in vitro. These substances are used to treat or
 CC prevent diseases associated with abnormal signal transduction pathways
 CC that involve the proteins, particularly cancer (e.g. leukaemia and
 CC lymphoma), while modulators of ALK-7 (which is a type I receptor
 CC serine/threonine kinase) are used to promote neuronal survival,
 CC particularly for treating Alzheimer's, Parkinson's or Huntington's
 CC diseases. Nucleic acid fragments of the polynucleotides encoding the
 CC proteins can be used as probes to identify and clone related sequences;
 CC to detect protein-encoded RNA; to generate transgenic animals and in gene
 CC therapy (optionally after mutation). Ab are used to determine the
 CC proteins
 XX
 XX Sequence 405 AA;

Query Match 100.0%; Score 1174; DB 2; Length 405;
 Best Local Similarity 100.0%; Pred. No. 9.9e-127;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QNRDKNRYDILPYDSTRVPLGKKNKYINASYIRIVNHEEYFYIATQGLPETIEDFWQ 60
 Db 188 QNRDKNRYDILPYDSTRVPLGKKNKYINASYIRIVNHEEYFYIATQGLPETIEDFWQ 247
 QY 61 MVLNENCNVAMITREIECGVIKCYSWPISLKEPLEFEHFSVLETFHVTQYTVRVFQ 120
 Db 248 MVLNENCNVAMITREIECGVIKCYSWPISLKEPLEFEHFSVLETFHVTQYTVRVFQ 307
 QY 121 IVKSTGKSCVQKHLQFTKPDHGTGPASADFFIKYVYVRKSHITGELLVHCSAGVGRGTG 180
 Db 308 IVKSTGKSCVQKHLQFTKPDHGTGPASADFFIKYVYVRKSHITGELLVHCSAGVGRGTG 367
 QY 181 VFICVDVVFSAIEKNYSFDMINIVTQMRKQRCGMIQTK 218
 Db 368 VFICVDVVFSAIEKNYSFDMINIVTQMRKQRCGMIQTK 405

RESULT 2
 AAW89249
 ID AAW89249 standard; protein; 426 AA.
 XX
 AC AAW89249;
 XX
 DT 10-MAR-1999 (first entry)
 XX
 DE Mouse PTP05.
 XX
 KW PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;
 KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;
 KW neurodegenerative disease; neuronal survival; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease.
 XX
 OS Mus sp.
 XX
 PN WO9849317-A2.
 XX
 PD 05-NOV-1998.
 XX
 PF 27-APR-1998; 98WO-US008439.
 PR 28-APR-1997; 97US-0044428P.
 PR 20-MAY-1997; 97US-0047222P.
 PR 11-JUN-1997; 97US-0049477P.
 PR 11-JUN-1997; 97US-0049756P.
 PR 18-JUN-1997; 97US-0049914P.
 PR 23-OCT-1997; 97US-0063595P.
 XX
 PA (SUGEN) SUGEN INC.

XX Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;
 PI Courtneidge SA, App H, Hui TH;
 PI WPI; 1999-009434/01.
 DR N-PSDB; AAW81744.
 DR

XX New nucleic acid encoding specific protein tyrosine phosphatases - useful
 PT for identifying specific modulators for treatment and prevention of
 PT cancer and neurodegenerative disease.
 XX
 XX Claim 2; Page 155-157; 193pp; English.

XX The present invention describes isolated, enriched or purified nucleic
 CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The
 CC present sequence represents mouse PTP05. The above proteins, other than
 CC ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify
 CC substances that modulate their activity (i.e. agonists and antagonists,
 CC including NBP) in vivo or in vitro. These substances are used to treat or
 CC prevent diseases associated with abnormal signal transduction pathways
 CC that involve the proteins, particularly cancer (e.g. leukaemia and
 CC lymphoma), while modulators of ALK-7 (which is a type I receptor
 CC serine/threonine kinase) are used to promote neuronal survival,
 CC particularly for treating Alzheimer's, Parkinson's or Huntington's
 CC diseases. Nucleic acid fragments of the polynucleotides encoding the
 CC proteins can be used as probes to identify and clone related sequences;
 CC to detect protein-encoded RNA; to generate transgenic animals and in gene
 CC therapy (optionally after mutation). Ab are used to determine the
 CC proteins
 XX
 XX Sequence 426 AA;

Query Match 100.0%; Score 1174; DB 2; Length 426;
 Best Local Similarity 100.0%; Pred. No. 1.1e-126;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QNRDKNRYDILPYDSTRVPLGKKNKYINASYIRIVNHEEYFYIATQGLPETIEDFWQ 60
 Db 188 QNRDKNRYDILPYDSTRVPLGKKNKYINASYIRIVNHEEYFYIATQGLPETIEDFWQ 247
 QY 61 MVLNENCNVAMITREIECGVIKCYSWPISLKEPLEFEHFSVLETFHVTQYTVRVFQ 120
 Db 248 MVLNENCNVAMITREIECGVIKCYSWPISLKEPLEFEHFSVLETFHVTQYTVRVFQ 307
 QY 121 IVKSTGKSCVQKHLQFTKPDHGTGPASADFFIKYVYVRKSHITGELLVHCSAGVGRGTG 180
 Db 308 IVKSTGKSCVQKHLQFTKPDHGTGPASADFFIKYVYVRKSHITGELLVHCSAGVGRGTG 367
 QY 181 VFICVDVVFSAIEKNYSFDMINIVTQMRKQRCGMIQTK 218
 Db 368 VFICVDVVFSAIEKNYSFDMINIVTQMRKQRCGMIQTK 405

RESULT 3
 AAW89250
 ID AAW89250 standard; protein; 463 AA.
 XX
 AC AAW89250;
 XX
 DT 10-MAR-1999 (first entry)
 XX
 DE Mouse PTP05 isoform #1.
 XX
 KW PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;
 KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;
 KW neurodegenerative disease; neuronal survival; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease.
 XX
 OS Mus sp.
 XX
 PN WO9849317-A2.
 XX
 PD 05-NOV-1998.
 XX
 PF 27-APR-1998; 98WO-US008439.
 PR 28-APR-1997; 97US-0044428P.
 PR 20-MAY-1997; 97US-0047222P.
 PR 11-JUN-1997; 97US-0049477P.

PR 11-JUN-1997; 97US-0049756P.
 PR 18-JUN-1997; 97US-0049914P.
 PR 23-OCT-1997; 97US-0063595P.
 XX
 XX (SUBG-) SUGEN INC.
 XX Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;
 PI Courtneidge SA, App H, Hui TH;
 XX WPI; 1999-009434/01.
 DR N-PSDB; AAV81745.
 XX
 XX New nucleic acid encoding specific protein tyrosine phosphatases - useful
 PT for identifying specific modulators for treatment and prevention of
 PT cancer and neurodegenerative disease.
 XX
 PS Claim 2; Page 157-158; 193pp; English.
 CC The present invention describes isolated, enriched or purified nucleic
 CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The
 CC present sequence represents mouse PTP05. The above proteins, other than
 CC ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify
 CC substances that modulate their activity (i.e. agonists and antagonists,
 CC including NBP) in vivo or in vitro. These substances are used to treat or
 CC prevent diseases associated with abnormal signal transduction pathways
 CC that involve the proteins, particularly cancer (e.g. leukaemia and
 CC lymphoma), while modulators of ALK-7 (which is a type I receptor
 CC serine/threonine kinase) are used to promote neuronal survival,
 CC particularly for treating Alzheimer's, Parkinson's or Huntington's
 CC diseases. Nucleic acid fragments of the polynucleotides encoding the
 CC proteins can be used as probes to identify and clone related sequences;
 CC to detect protein-encoded RNA; to generate transgenic animals and in gene
 CC therapy (optionally after mutation). Ab are used to determine the
 CC proteins
 XX
 SQ Sequence 463 AA;
 Query Match 100.0%; Score 1174; DB 2; Length 463;
 Best Local Similarity 100.0%; Pred. No. 1.2e-126;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPTIEDFWQ 60
 Db 225 QNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPTIEDFWQ 284
 QY 61 MVLNNCNVIAITREIECGVIKCYWPISLKEPFEHFSVLETFHVTQVTVRVFQ 120
 Db 285 MVLNNCNVIAITREIECGVIKCYWPISLKEPFEHFSVLETFHVTQVTVRVFQ 344
 QY 121 IVKSTGKSCQVKHLQFTKWDHGTTPASADFFIKYRVYRKSHITGPLLVHCSAGVGRG 180
 Db 345 IVKSTGKSCQVKHLQFTKWDHGTTPASADFFIKYRVYRKSHITGPLLVHCSAGVGRG 404
 QY 181 VFCVDVFSALEKNYSFDMNIVTQMRKQRCGMIOTK 218
 Db 405 VFCVDVFSALEKNYSFDMNIVTQMRKQRCGMIOTK 442
 RESULT 4
 ID AAE37994
 XX AAE37994 standard; protein; 261 AA.
 AC AAE37994;
 XX
 DT 06-NOV-2003 (first entry)
 XX Human kinase and phosphatase (kpp-39) protein.
 DE
 XX Human; kinase; phosphatase; kpp; cell proliferative disorder; hepatitis;
 KW atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer;
 KW psoriasis; thrombocytopenia; developmental disorder; Reiter's syndrome;
 KW renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease;
 KW neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis;

KW autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome;
 KW acquired immune deficiency syndrome; immunosuppressive; Crohn's disease;
 KW neutropenic; dermatitis; multiple sclerosis; diabetes mellitus;
 KW allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome;
 KW osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological;
 KW gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.
 XX
 OS Homo sapiens.
 XX
 PN WO2003050084-A2.
 XX
 PD 19-JUN-2003.
 XX
 PF 06-DEC-2002; 2002WO-US039126.
 XX
 PR 07-DEC-2001; 2001US-0340235P.
 PR 19-DEC-2001; 2001US-0343007P.
 PR 21-DEC-2001; 2001US-0343546P.
 PR 04-FEB-2002; 2002US-0354388P.
 PR 15-FEB-2002; 2002US-0357675P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Kable AE, Chien D, Wilson AD, Swarnakar A, Gorvad AE;
 PI Hafalia AJA, Emerling BM, Rankumar J, Jin P, Griffin JA, Marquis JP;
 PI Baughn WR, Chawla NK, Lehr-Mason PM, Knare R, Lee S, Hawkins PR;
 PI Becha SD, Lee SY, Sprague WW, Zebarjadian Y;
 XX WPI; 2003-532894/50.
 DR N-PSDB; AAD57366.
 DR
 DR New human kinases and phosphatases and polynucleotides, useful for
 XX diagnosing, treating or preventing autoimmune or inflammatory disorders
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
 PT cancer or hepatitis.
 PT
 XX
 PS Claim 1; Page 242; 282pp; English.

XX The invention relates to an isolated polypeptide, which is a human kinase
 CC and phosphatase (KPP). KPP agonists and antagonists are useful for
 CC diagnosing, treating or preventing disorders associated with aberrant
 CC expression of KPP, particularly cell proliferative disorders (e.g.
 CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal
 CC nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary
 CC thrombocytopenia or cancer), developmental disorders (eg. renal tubular
 CC acidosis, anaemia or mental retardation), neurological disorders (e.g.
 CC Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/
 CC inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome,
 CC allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's
 CC disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,
 CC gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome,
 CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
 CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
 CC bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP
 CC is useful in assessing the effects of exogenous compounds on the
 CC expression of nucleic acids and kinases and phosphatases. KPP gene is
 CC useful in gene therapy and for creating transgenic animals to model human
 CC disease. The present sequence is human KPP protein
 XX
 SQ Sequence 261 AA;

Query Match 79.7%; Score 936; DB 6; Length 261;
 Best Local Similarity 78.8%; Pred. No. 2e-99;
 Matches 171; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

QY 2 NRDKNRYDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPTIEDFWQ 61
 Db 24 NREKNRYDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPTIEDFWQ 83
 QY 62 VLENNCNVIAITREIECGVIKCYWPISLKEPFEHFSVLETFHVTQVTVRVFQ 121
 Db 84 VLENNCNVIAITREIECGVIKCYWPISLKEPFEHFSVLETFHVTQVTVRVFQ 143

QY 122 VKSTGKSCVXHLQFTKWPDHGTPASADFFIKYVYVVKSHITGTLVHCSAGVGTGV 181
 Db 144 VEKSTGTSVSKQLQFTKWPDHGTPASADFFIKYVYVVKSHITGTLVHCSAGVGTGV 203
 QY 182 FLCVDVVFSAIEKNYSFDMNIVTQMKRCGMIQTK 218
 Db 204 FLCVDVVFCAIVKNCNFMNDIVAQMREQRSGMVQTK 240

RESULT 5

ID AAE37996 standard; protein; 412 AA.

XX AAE37996;

XX 06-NOV-2003 (first entry)

XX Human kinase and phosphatase (KPP-41) protein.

XX Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis;
 KW atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer;
 KW psoriasis; thrombocytopenia; developmental disorder; Reiter's syndrome;
 KW renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease;
 KW neurological disorder; Parkinson's disease; epilepsy; Glomerulonephritis;
 KW autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome;
 KW acquired immune deficiency syndrome; immunosuppressive; Crohn's disease;
 KW noctropic; transgenic; dermatitis; multiple sclerosis; diabetes mellitus;
 KW allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome;
 KW osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological;
 KW gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.

XX Homo sapiens.

XX WO2003050084-A2.

XX 19-JUN-2003.

XX 06-DEC-2002; 2002WO-US039126.

XX 07-DEC-2001; 2001US-0340235P.

XX 19-DEC-2001; 2001US-0343007P.

XX 21-DEC-2001; 2001US-0343546P.

XX 04-FEB-2002; 2002US-0354388P.

XX 15-FEB-2002; 2002US-0357675P.

XX (INCY-) INCYTE GENOMICS INC.

XX Kable AE, Chien D, Wilson AD, Swarnakar A, Gorvad AE;

XX Hafalia AJA, Emerling BM, Ramkumar J, Jin P, Griffin JA, Marquis JP;

XX Baughn MR, Chawla NK, Lehr-Mason PW, Khare R, Lee S, Hawkins PR;

XX Becha SD, Lee SY, Sprague WW, Zebarjadian Y;

XX WPI; 2003-532894/50.

XX N-PSDB; AAD57368.

XX New human kinases and phosphatases and polynucleotides, useful for
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
 PT cancer or hepatitis.

XX Claim 1; Page 243-244; 282pp; English.

XX The invention relates to an isolated polypeptide, which is a human kinase
 CC and phosphatase (KPP). KPP agonists and antagonists are useful for
 CC diagnosing, treating or preventing disorders associated with aberrant
 CC expression of KPP, particularly cell proliferative disorders (e.g.
 CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal
 CC nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary
 CC thrombocytopenia or cancer), developmental disorders (eg. renal tubular
 CC acidosis, anaemia or mental retardation), neurological disorders (e.g.
 CC Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/
 CC inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome,
 CC allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's

CC disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,
 CC gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome,
 CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
 CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
 CC bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP
 CC is useful in assessing the effects of exogenous compounds on the
 CC expression of nucleic acids and kinases and phosphatases. KPP gene is
 CC useful in gene therapy and for creating transgenic animals to model human
 CC disease. The present sequence is human KPP protein

XX Sequence 412 AA;

Query Match 79.7%; Score 936; DB 6; Length 412;

Best Local Similarity 78.8%; Pred. No. 3.8e-99;

Matches 171; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

QY 2 NRDKNRYRDLIPYDSTRVPLGKKNKYINASYIRIVNHEEYFYIATQGPLTIEDFWQM 61

Db 183 NREKNRYRDLIPYDSTRVPLGKKNKYINASYIRIVNCGEYFYIATQGPLTIEDFWQM 242

QY 62 VLENNCNVIAITRETECGVICKSYWPISLKEPLEFEHFSVLETFHVTQYFTRVFI 121

Db 243 VLENNCNVIAITRETECGVICKSYWPISLKEPLEFEHFSVLETFHVTQYFTRVFI 302

QY 122 VKSTGKSCVXHLQFTKWPDHGTPASADFFIKYVYVVKSHITGTLVHCSAGVGTGV 181

Db 303 VEKSTGTSVSKQLQFTKWPDHGTPASADFFIKYVYVVKSHITGTLVHCSAGVGTGV 362

QY 182 FLCVDVVFSAIEKNYSFDMNIVTQMKRCGMIQTK 218

Db 363 FLCVDVVFCAIVKNCNFMNDIVAQMREQRSGMVQTK 399

RESULT 6

AAE14454

ID AAE14454 standard; protein; 420 AA.

XX AAE14454;

XX 26-MAR-2002 (first entry)

XX Human protein phosphatase-4.

XX Human; protein phosphatase; PP-4; immune system disorder; AIDS; allergy;
 KW neurological disorder; developmental disorder; Alzheimer's disease;
 KW cell proliferative disorder; Huntington's disease; arteriosclerosis;
 KW renal tubular acidosis; gonadal dysgenesis; cancer; adenocarcinoma;
 KW leukaemia; transgenic animal; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 183..411

XX Active-site /note= "Protein-tyrosine phosphatase"

XX /note= "Tyrosine specific protein phosphatase active site"

XX Region 351..363

XX Domain /note= "Tyr_phosphatase"

XX /label= Transmembrane_domain

XX WO200196546-A2.

XX 20-DEC-2001.

XX 14-JUN-2001; 2001WO-US019442.

XX 16-JUN-2000; 2000US-0212447P.

XX 22-JUN-2000; 2000US-0213746P.

XX 29-JUN-2000; 2000US-0215210P.

XX 06-JUL-2000; 2000US-0216529P.

XX 12-JUL-2000; 2000US-0218080P.

```
PR 21-JUL-2000; 2000US-0220117P.
XX (INCY-) INCYTE GENOMICS INC.
PA
XX
XX Au-Young J, Baughn MR, Lee L, Elliott VS, Gandhi AR, Griffin JA,
PI Hafalia A, Kearney L, Lee EA, Lu Y, Nguyen DB, Patterson C;
PI Ramkumar J, Reddy R, Sanjanwala MS, Stewart EA, Tang YT, Thornton M;
PI Tribouley CM, Wallia NK, Yang J, Yao MG, Yue H;
XX
XX WPI; 2002-090206/12.
DR N-PSDB; AAD24022.
XX
XX Novel polypeptide, useful for diagnosing, treating or preventing
PT disorders of growth and development, immune system, neurological and cell
PT proliferation diseases, comprises cancer protein phosphatase
PT polypeptides.
XX
XX Claim 1; Page 105-106; 116pp; English.
XX
XX The present sequence is human protein phosphatase (PP)-4. PP
XX polynucleotide and polypeptide are useful in the diagnosis, treatment and
XX prevention of immune system disorders, neurological disorders,
XX developmental disorders and cell proliferative disorders. Examples of
XX immune system disorders include acquired immune deficiency syndrome
XX (AIDS), severe combined immunodeficiency disease (SCID), adult
XX respiratory distress syndrome, allergies, amyloidosis, anaemia, asthma,
XX atherosclerosis, Crohn's disease, atopic dermatitis, diabetes mellitus,
XX emphysema, Goodpasture's syndrome, gout, Graves' disease, multiple
XX sclerosis, myasthenia gravis, myocardial or pericardial inflammation,
XX osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
XX rheumatoid arthritis, Sjogren's syndrome, scleroderma, systemic
XX sclerosis, trauma; neurological disorders include Alzheimer's disease,
XX Huntington's disease, dementia, epilepsy, Parkinson's disease, mental
XX retardation and other developmental disorders of central nervous system
XX such as Down's syndrome, cerebral palsy, periodic paralysis, mental
XX disorders including mood, anxiety, and schizophrenic disorders, seasonal
XX affective disorder such as akathisia, amnesia, catatonia, dyskinesia;
XX developmental disorders include e.g. renal tubular acidosis, Duchenne and
XX Becker muscular dystrophy, gonadal dysgenesis, hypothyroidism; cell
XX proliferative disorders include e.g. actinic keratosis, arteriosclerosis,
XX atherosclerosis, bursitis, cirrhosis, hepatitis, psoriasis and cancer
XX including adenocarcinoma, leukaemia. The polypeptide and polynucleotide
XX are further useful for analysing proteome of a tissue or a cell type, for
XX screening an agonist/antagonist, a compound that specifically binds to it
XX or its modulator. The polynucleotide is useful for creating knockin
XX humanised animals (pigs) or transgenic animals (mice or rats) to model
XX human disease, for generating a transcript image of a tissue or cell
XX type, which represents the global pattern of gene expression by a
XX particular tissue or cell type
XX
XX Sequence 420 AA;
SQ
Query Match 79.7%; Score 936; DB 5; Length 420;
Best Local Similarity 78.8%; Pred. No. 3.9e-99;
Matches 171; Conservative 22; Mismatches 24; Indels 0; Gaps 0;
QY 2 NRDKNRYRDLPLVDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQM 61
Db 183 NREKNRYRDLPLVDSTRVPLGSKDYINASYIRIVNCGEYFYIATQGPLLLTIDDFWQM 242
QY 62 VLENNCNVIAMITREIECGVIKCYSWYPISLKQPLEFHFVSFLETFHTQYFTRVFOI 121
Db 243 VLENNNSVIAMITREIEGGIKCYHYWPISLKQPLELKHFRVPLENYQIILFIIRFQV 302
QY 122 VKKSTGKSCVKHLQFTKWPDHGTPASADFFIKYRVYVRKSHITGPLLHVCASGVGRTGV 181
Db 303 VEKSTGTSHSVKQLQFTKWPDHGTPASADSFYIKYRVYRKSHTLTPGVHVCASGAGTGV 362
QY 182 FICVDVVFSAIEKNYSPDINNIYVTKMRKQRCGMIOTK 218
Db 363 FLCVDVVFCAIVKNCNFIIMDIVAQMREQRSGMVQTK 399
```

```
RESULT 7
ABG30845
ID ABG30845 standard; protein; 398 AA.
XX
XX ABG30845;
AC
XX 21-OCT-2002 (first entry)
DT
XX Human tyrosine phosphatase protein #1.
XX
XX Human; tyrosine phosphatase; obesity; diabetes; Parkinson's disease;
XX central nervous system disorder; CNS; cardiovascular disorder; stroke;
XX chronic obstructive pulmonary disease; cancer; multiple sclerosis;
XX Alzheimer's disease; Huntington's disease; congestive heart failure;
XX myocardial infarction; chromosome 10.
XX
XX Homo sapiens.
OS
XX
XX WO200242435-A2.
PN
XX
XX 30-MAY-2002.
XX
XX 27-NOV-2001; 2001WO-EP013794.
PF
XX
XX 27-NOV-2000; 2000US-0252912P.
PR
XX (FARB ) BAYER AG.
PA
XX
XX Zhu Z;
XX
XX WPI; 2002-575236/61.
XX N-PSDB; ABK89178.
XX
XX New human tyrosine phosphatase polypeptide, the regulation of which is
XX useful for treating obesity, diabetes, cardiovascular or central nervous
XX system disorder, chronic obstructive pulmonary disease and cancer.
XX
XX Claim 25; Fig 2; 145pp; English.
XX
XX The present invention relates to a new human tyrosine phosphatase
XX polypeptide. The invention is useful for the preparation of a medicament
XX for modulating the activity of human tyrosine phosphatase in a disease
XX such as obesity, diabetes, a central nervous system (CNS) disorder,
XX chronic obstructive pulmonary disease, cardiovascular disorder or cancer.
XX The invention is useful for treating a human tyrosine phosphatase
XX dysfunction related disease, preferably the above mentioned diseases. The
XX invention is useful for treating the above mentioned disorders, where the
XX CNS disorder is selected from Parkinson's disease, multiple sclerosis,
XX stroke, Alzheimer's disease, and Huntington's disease, and the
XX cardiovascular disorder is selected from congestive heart failure and
XX myocardial infarction. The molecules of the invention are useful in
XX diagnostic assays for detecting diseases and abnormalities or
XX susceptibility to disease and abnormalities related to the presence of
XX mutations in the polynucleotide coding the polypeptide of the invention.
XX The present amino acid sequence represents the human tyrosine phosphatase
XX protein #1 of the invention. This sequence is encoded by the human
XX tyrosine phosphatase gene located on chromosome 10
XX
XX Sequence 398 AA;
SQ
Query Match 79.0%; Score 928; DB 5; Length 398;
Best Local Similarity 77.9%; Pred. No. 3e-98;
Matches 169; Conservative 24; Mismatches 24; Indels 0; Gaps 0;
QY 2 NRDKNRYRDLPLVDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQM 61
Db 161 NREKNRYRDLPLVDSTRVPLGSKDYINASYIRIVNCGEYFYIATQGPLLLTIDDFWQM 220
QY 62 VLENNCNVIAMITREIECGVIKCYSWYPISLKQPLEFHFVSFLETFHTQYFTRVFOI 121
Db 221 VLENNNSVIAMITREIEGGIKCYHYWPISLKQPLELKHFRVPLENYQIILFIIRFQV 280
QY 122 VKKSTGKSCVKHLQFTKWPDHGTPASADFFIKYRVYVRKSHITGPLLHVCASGVGRTGV 181
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Db 281 VEXSTGTSVSHVQLQFTKWPDPHGTPASADSFYIKYIRYARKSHLTGPMVHCSAGIGRTGV 340
QY 182 FICVDVVFSAIEKNYSFDMNIVTOMRKORCGMIQTK 218
Db 341 FLCVDVVFCAIVKDCSFNMDIVAQMREQRSGMWQTK 377

RESULT 8
ADD89795
ID ADD89795 standard; protein; 398 AA.
XX ADD89795;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human DKEZP56K0524 protein SEQ ID NO:10.
XX
XX cancer associated phosphatase; enzyme; human; cancer; tumour; cytostatic;
KW immunosuppressive; antidiabetic; neuroprotective; antirheumatic;
KW antiarthritic; antipsoriatic; antiarteriosclerotic; antinflammatory;
KW vulnary; gynaecological; antiangiogenic; hyperproliferative disease;
KW autoimmune disease; diabetes mellitus; multiple sclerosis;
KW rheumatoid arthritis; psoriasis; atherosclerosis; inflammation; scarring;
KW endometriosis; angiogenesis.
XX
XX Homo sapiens.
XX
XX WO2003083102-A2.
XX
XX 09-OCT-2003.
XX
XX 19-MAR-2003; 2003WO-CA000393.
XX
XX 28-MAR-2002; 2002US-0368859P.
XX
XX (KINE-) KINETEK PHARM INC.
XX
XX Delaney AD;
XX
XX WPI; 2003-902934/82.
XX
XX N-PSDB; ADD89794.
XX
XX
XX New nucleic acids encoding cancer associated phosphatases, useful as
PT targets for screening pharmaceutical agents that inhibit the growth of
PT tumor cells, or for diagnosing and treating cancer, inflammation or
PT autoimmune disease.
XX
XX Claim 1; SEQ ID NO 10; 63pp; English.
XX

The present invention describes an isolated cancer associated phosphatase nucleic acid. Also described: (1) a method of screening for biologically active agents that modulate a cancer associated phosphatase function; (2) a method for the diagnosis of cancer; (3) a method for inhibiting the growth of a cancer cell; (4) methods of screening for targets of a cancer associated phosphatase, where the targets are associated with signal transduction in cancer cells; (5) a compound (C) for the treatment of a tumour; (6) a composition for the treatment of a tumour comprising a pharmaceutical carrier and (C); (7) methods for treating a tumour; and (8) a method for visualising a tumour in a patient. A cancer associated phosphatase of the present invention has cytostatic, immunosuppressive, antidiabetic, neuroprotective, antirheumatic, antiarthritic, antipsoriatic, antiarteriosclerotic, antinflammatory, vulnary, gynaecological and antiangiogenic activities. The cancer associated phosphatases and nucleic acids encoding the proteins are useful for visualising tumours in patients or diagnosing and treating cancer, e.g. pancreas, lung, ovarian, liver or colon cancer. The polypeptides and nucleic acids may also be used for treating hyperproliferative diseases, such as autoimmune disease, diabetes mellitus, multiple sclerosis, rheumatoid arthritis, psoriasis, atherosclerosis, inflammation, scarring, endometriosis or angiogenesis, determining the effectiveness of drugs, determining patient prognosis, or as targets for screening pharmaceutical agents that inhibit the growth or metastasis of tumour cells. The present

CC sequence represents the human cancer associated phosphatase
CC DKFZP56K0524, which is used in the exemplification of the present
CC invention.
XX
XX SQ Sequence 398 AA;
Query Match 79.0%; Score 928; DB 7; Length 398;
Best Local Similarity 77.9%; Pred. NO. 3e-98;
Matches 169; Conservative 24; Mismatches 24; Indels 0; Gaps 0;
QY 2 NRDKNRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQM 61
Db 161 NREKNRYRDLIPYDSTRVPLGSKDYINASYIRIVNCGEYFYIATQGPLLSTIDFWQM 220
QY 62 VLENNCNVIAITREIECGVIKCYSWPISLKEPFEHFSVELETFHVTQYFVRFQI 121
Db 221 VLENNCNVIAITREIEGGIICVHYWPIISLKEPFEHFSVELETFHVTQYFVRFQI 121
QY 122 VKSTGKSCVCKHLQFTKWPDPHGTPASADSFYIKYIRYARKSHLTGPMVHCSAGIGRTGV 181
Db 281 VEXSTGTSVSHVQLQFTKWPDPHGTPASADSFYIKYIRYARKSHLTGPMVHCSAGIGRTGV 340
QY 182 FICVDVVFSAIEKNYSFDMNIVTOMRKORCGMIQTK 218
Db 341 FLCVDVVFCAIVKDCSFNMDIVAQMREQRSGMWQTK 377

RESULT 9
ADE09123
ID ADE09123 standard; protein; 409 AA.
XX
XX AC ADE09123;
XX
XX DT 29-JAN-2004 (first entry)
XX
XX DE Novel protein-related contig polypeptide sequence #189.
XX
XX KW novel gene; novel protein; tissue marker; molecular weight marker;
KW chromosome marker; genetic disorder; contig.
XX
XX OS Unidentified.
XX
XX PN WO2003054152-A2.
XX
XX PD 03-JUL-2003.
XX
XX PF 10-DEC-2002; 2002WO-US039555.
XX
XX PR 10-DEC-2001; 2001US-0339739P.
XX
XX PR 11-DEC-2001; 2001US-0339453P.
XX
XX PR 14-MAR-2002; 2002US-0365091P.
XX
XX PR 14-MAR-2002; 2002US-0365384P.
XX
XX PR 12-APR-2002; 2002US-0372381P.
XX
XX PR 12-APR-2002; 2002US-0372615P.
XX
XX PR 22-APR-2002; 2002US-00128558.
XX
XX PR 24-APR-2002; 2002US-0376045P.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX
XX WPI; 2003-569235/53.
XX
XX New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.
XX
XX Disclosure; SEQ ID NO 2667; 1177pp; English.
XX
XX The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:

CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present amino acid sequence was used in the
CC exemplification of the invention.
XX
SQ Sequence 409 AA;

Query Match 79.0%; Score 928; DB 7; Length 409;
Best Local Similarity 77.9%; Pred. No. 3.1e-98;
Matches 169; Conservative 24; Mismatches 24; Indels 0; Gaps 0;

QY 2 NRDNRYRDLDPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATGGLPETIEDFWQM 61
DB 172 NREKNRYRDLDPYDSTRVPLGKNDYINASYIRIVNCGEYFYIATGGLSTIDDFWQM 231
QY 62 VLENNCNVIAITREIECGVIKCYWPIISLKEPLEFEHFSVLETPHVTQYFTVRVFOI 121
DB 232 VLENNSNVIAITREMEGGIICVHYWPIISLKEPLELKHFRVFLFNQYIILQYFIIRMFQV 291
QY 122 VKKSTGKSCQVKKHLOFTKWDHGTDPASADPFIKYVRYVRKSHITGPLLHVCAGVGRGTG 181
DB 292 VEKSTGTSHSVKQLQFTKWDHGTDPASADSFYIKYRYARKSHLTGPMVHVCAGIGRTGV 351
QY 182 FICVDVVFSIAEKYNSFDIMNIVTOMRKORCGMIQTK 218
DB 352 FLCVDVVFCALVKDCSFNIMDIVAQMREQRSGMWQTK 388

RESULT 10
ADE08106
ID ADE08106 standard; protein; 508 AA.
AC ADE08106;
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel protein (useful for identifying genetic disorders) #261.
XX
KW novel gene; novel protein; tissue marker; molecular weight marker;
KW chromosome marker; genetic disorder.
XX
OS Unidentified.
XX
PN WO2003054152-A2.
XX
PD 03-JUL-2003.
XX
PF 10-DEC-2002; 2002WO-US039555.
XX
PR 10-DEC-2001; 2001US-0339739P.
PR 11-DEC-2001; 2001US-0339453P.
PR 14-MAR-2002; 2002US-0365091P.
PR 14-MAR-2002; 2002US-0365384P.
PR 12-APR-2002; 2002US-0372381P.
PR 12-APR-2002; 2002US-0372615P.
PR 22-APR-2002; 2002US-00128558.
PR 24-APR-2002; 2002US-0376045P.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX
DR WPI; 2003-569235/53.
DR N-PSDB; ADE07195.
XX
PT New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.
XX

PS Claim 20; SEQ ID NO 1172; 1177pp; English.
XX
CC The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present amino acid sequence represents a protein
CC of the invention.
XX
SQ Sequence 508 AA;

Query Match 79.0%; Score 928; DB 7; Length 508;
Best Local Similarity 77.9%; Pred. No. 4.3e-98;
Matches 169; Conservative 24; Mismatches 24; Indels 0; Gaps 0;

QY 2 NRDNRYRDLDPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATGGLPETIEDFWQM 61
DB 271 NREKNRYRDLDPYDSTRVPLGKNDYINASYIRIVNCGEYFYIATGGLSTIDDFWQM 330
QY 62 VLENNCNVIAITREIECGVIKCYWPIISLKEPLEFEHFSVLETPHVTQYFTVRVFOI 121
DB 331 VLENNSNVIAITREMEGGIICVHYWPIISLKEPLELKHFRVFLFNQYIILQYFIIRMFQV 390
QY 122 VKKSTGKSCQVKKHLOFTKWDHGTDPASADPFIKYVRYVRKSHITGPLLHVCAGVGRGTG 181
DB 391 VEKSTGTSHSVKQLQFTKWDHGTDPASADSFYIKYRYARKSHLTGPMVHVCAGIGRTGV 450
QY 182 FICVDVVFSIAEKYNSFDIMNIVTOMRKORCGMIQTK 218
DB 451 FLCVDVVFCALVKDCSFNIMDIVAQMREQRSGMWQTK 487

RESULT 11
ABG06042
ID ABG06042 standard; protein; 561 AA.
XX
AC ABG06042;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #6033.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS70229.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 36401; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)

sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic amino acid sequences in the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 561 AA;
Query Match 79.0%; Score 928; DB 4; Length 561;
Best Local Similarity 77.9%; Pred. No. 4.9e-98;
Matches 169; Conservative 24; Mismatches 24; Indels 0; Gaps 0;
QY 2 NRDKNRYDILPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLTIEDFWQM 61
Db 324 NREKNRYDILPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLTIEDFWQM 383
QY 62 VLENNVMIATREIEGCVTKCSYWPISLKEPLEHFSVLETHVTFYFVRVFI 121
Db 384 VLENNVMIATREIEGCVTKCSYWPISLKEPLEHFSVLETHVTFYFVRVFI 443
QY 122 VKSTGSKQCVKHLQFTKWPDPHGTPASADFFIKYVYVRKSHITGPIIVHCSAGVGTGV 181
Db 444 VERSTGSHSVKQJQFTKWPDPHGTPASADFFIKYVYVRKSHITGPIIVHCSAGVGTGV 503
QY 182 FICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIOQTK 218
Db 504 FLCVDVVFCAIVKDCSFNIMDIVAQMRBQSGMVQTK 540

RESULT 12
ADK71863
ID ADK71863 standard; protein; 348 AA.
XX ADK71863;
XX 20-MAY-2004 (first entry)
XX Human kinase and phosphatase KPP-40 protein.
XX human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic;
KW hypotensive; vasotrophic; antiinflammatory; antiangiinal; anti-HIV;
KW antiallergic; antiasthmatic; immunosuppressive; antithyroid;
KW dermatological; antidiabetic; nephrotropic; angiotensin; gastrointestinal;
KW neuroprotective; osteoporotic; antiarthritic; urapathic; ophthalmological;
KW antirheumatic; antiparkinsonian; nootropic; anticonvulsant; hepatotropic;
KW antipsoriatic; haemostatic; cytostatic; antilipemic; antiparasitic;
KW antihelminthic; antibacterial; virucide; protozoacide; fungicide;
KW cardiovascular disease; immune system; neurological; growth; development;
KW cell proliferation; viral; bacterial; fungal; parasitic; protozoan;
KW helminthic infection; transgenic; gene therapy; enzyme.
XX Homo sapiens.
XX WO2004018641-A2.
XX 04-MAR-2004.
XX 25-AUG-2003; 2003WO-US026635.
XX

XX 26-AUG-2002; 2002US-0406172P.
PR 25-SEP-2002; 2002US-041310P.
PR 27-SEP-2002; 2002US-0414296P.
XX 11-OCT-2002; 2002US-0417821P.
XX (INCY-) INCYTE CORP.
XX Baughn MR, Richardson TW, Marquis JP, Swarnakar A, Tang YT;
PI Becha SD, Emerling BM, Jin P, Wilson AD, Yue H, Gietzen KJ;
PI Chang H, Yang YG, Lee SY, Khare R, Elliott VS, Hafalia AJA;
PI Chawla NK, Ramkumar J, Gururajan R, Tribouley CM, Chien D, Tran UK;
PI Murage J;
XX WPI; 2004-226830/21.
DR N-PSDB; ADK71922.
XX New human kinases and phosphatases, useful for diagnosing, treating or
PT preventing atherosclerosis, hypertension, AIDS, allergy, multiple
PT sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
PT or hepatitis.
XX Claim 1; SEQ ID NO 40; 347pp; English.

The invention relates to a novel isolated polypeptide which is a human kinase and phosphatase (KPP). The polypeptide of the invention demonstrates cardiovascular, antiarteriosclerotic, hypotensive, vasotropic, antiinflammatory, antiangiinal, anti-HIV, antiallergic, antiasthmatic, immunosuppressive, antithyroid, dermatological, antidiabetic, nephrotropic, angiotensin, ophthalmological, antirheumatic, osteoporotic, antiarthritic, urapathic, anticonvulsant, antihelminthic, antiparkinsonian, nootropic, antilipemic, antiparasitic, antihelminthic, haemostatic, cytostatic, antiparasitic and fungicidal activities. The antibacterial, virucide, protozoacide and fungicidal activities. The kinase and phosphatase (KPP) polynucleotides, polypeptides, agonists and antagonists may be useful for diagnosing, treating or preventing disorders such as cardiovascular diseases, immune system disorders, neurological disorders, disorders affecting growth and development, cell proliferative disorders and viral, bacterial, fungal, parasitic, protozoan or helminthic infections. Furthermore, the molecules of the invention may be useful for creating transgenic animals to model human disease and during gene therapy. The current sequence is that of a human KPP protein of the invention.

Sequence 348 AA;
Query Match 48.7%; Score 572; DB 8; Length 348;
Best Local Similarity 52.5%; Pred. No. 4.3e-57;
Matches 114; Conservative 16; Mismatches 15; Indels 72; Gaps 1;
QY 2 NRDKNRYDILPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLTIEDFWQM 61
Db 183 NREKNRYDILPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLTIEDFWQM 242
QY 62 VLENNVMIATREIEGCVTKCSYWPISLKEPLEHFSVLETHVTFYFVRVFI 121
Db 243 VLENNVMIATREIEGCVTKCSYWPISLKEPLEHFSVLETHVTFYFVRVFI 302
QY 122 VKSTGSKQCVKHLQFTKWPDPHGTPASADFFIKYVYVRKSHITGPIIVHCSAGVGTGV 181
Db 303 VEK-----
QY 182 FICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIOQTK 218
Db 306 -----SFNIMDIVAQMRBQSGMVQTK 327

RESULT 13
AAW89252
ID AAW89252 standard; protein; 122 AA.
XX AAW89252;
XX

DT 10-MAR-1999 (first entry)
 DE Rat PTP10.
 XX PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;
 KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;
 KW neurodegenerative disease; neuronal survival; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease.
 XX Rattus sp.
 OS
 XX WO9849317-A2.
 PN
 XX 05-NOV-1998.
 PD
 XX 27-APR-1998; 98WO-US008439.
 PF
 XX 28-APR-1997; 97US-0044428P.
 PR 20-MAY-1997; 97US-0047222P.
 PR 11-JUN-1997; 97US-0049477P.
 PR 11-JUN-1997; 97US-0049756P.
 PR 18-JUN-1997; 97US-0049914P.
 PR 23-OCT-1997; 97US-0063595P.
 XX (SUGEN-) SUGEN INC.
 PA
 XX Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;
 PI Courtnedge SA, App H, Hui TH;
 XX WPI; 1999-009434/01.
 DR N-PSDB; AAV81747.
 XX
 DR New nucleic acid encoding specific protein tyrosine phosphatases - useful
 PT for identifying specific modulators for treatment and prevention of
 PT cancer and neurodegenerative disease.
 XX
 XX Claim 2; Page 160; 193pp; English.
 PS
 XX The present invention describes isolated, enriched or purified nucleic
 CC acids encoding PTP04, SAD, PTP05, ALP and ALK-7 proteins. The
 CC present sequence represents rat PTP10. The above proteins, other than ALK
 CC -7, are protein tyrosine phosphatases (PTPs) and are used to identify
 CC substances that modulate their activity (i.e. agonists and antagonists,
 CC including NRP) in vivo or in vitro. These substances are used to treat or
 CC prevent diseases associated with abnormal signal transduction pathways
 CC that involve the proteins, particularly cancer (e.g. leukaemia and
 CC lymphoma), while modulators of ALK-7 (which is a type I receptor
 CC serine/threonine kinase) are used to promote neuronal survival,
 CC particularly for treating Alzheimer's, Parkinson's or Huntington's
 CC diseases. Nucleic acid fragments of the polynucleotides encoding the
 CC proteins can be used as probes to identify and clone related sequences;
 CC to detect protein-encoded RNA; to generate transgenic animals and in gene
 CC therapy (optionally after mutation). Ab are used to determine the
 CC proteins
 XX
 SQ Sequence 122 AA;
 Query Match 48.2%; Score 566; DB 2; Length 122;
 Best Local Similarity 83.6%; Pred. No. 4.7e-57;
 Matches 102; Conservative 7; Mismatches 13; Indels 0; Gaps 0;
 QY 57 DFQMWLENNCNVIAITREIEGCVIKCYSWPISLKEPLEPHEFVLETHVQYFTV 116
 DB 1 DFMGMWNNCNVIAITREIEGCVIKCCSWPVSLEKPLEPHEFVLETHVQYFTV 60
 QY 117 RVFQIVKSTGKSCQVKHLQFTKWPDPHGTPASADFFIKVYRVKSHITGPLLHVCSAGV 176
 DB 61 RIFQIVKSTGKSHVKGHLQFIKWPDPHGTPASVDFFIKIVYRVKSHITGPLLHVCTAGV 120
 QY 177 GR 178
 DB 121 GR 122

RESULT 14

ABU70688
 ID ABU70688 standard; protein; 766 AA.
 XX
 AC ABU70688;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Human adipocyte Selected Interacting domain, SID, #319.
 XX
 KW Human; prey; adipocyte; SID; selected interacting domain; anorectic;
 KW antidiabetic; protein-protein interaction; diabetes;
 KW yeast 2-hybrid assay; metabolic disorder; obesity.
 XX
 OS Homo sapiens.
 XX
 XX WO200286122-A2.
 PN
 XX 31-OCT-2002.
 PD
 XX 14-MAR-2002; 2002WO-EP003768.
 PF
 XX 14-MAR-2001; 2001US-0275734P.
 PR
 XX (HYBR-) HYBRIGENICS.
 PA
 XX Legrain P, Daviet L;
 PI
 XX WPI; 2003-103412/09.
 DR N-PSDB; ACAS7232.
 DR
 XX
 PT New complex between two interacting proteins in adipocyte cells, useful
 PT for identifying selected interacting domains that modulate protein
 PT interactions, or for preventing or treating metabolic disorders such as
 PT obesity or diabetes.
 XX
 PS Claim 6; Page 208-209; 382pp; English.
 CC
 CC The invention relates to a complex between two interacting proteins in
 CC adipocyte cells, given in the specification. The proteins are identified
 CC by selecting a bait protein from a known adipocyte marker and then
 CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by
 CC members of an adipocyte cDNA library. The proteins are designated SID
 CC (RTM) (selected interacting domains) proteins. Also included are a
 CC polynucleotide encoding a polypeptide in the adipocyte cells, a
 CC recombinant host cell expressing at least one of the interacting
 CC polypeptides of the complex, selecting a modulating compound in adipocyte
 CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid
 CC sequences given in the specification (including its fragment or variant),
 CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences
 CC given in the specification (including its fragment or variant), a vector
 CC comprising the SID (RTM) polynucleotide, a recombinant host cell
 CC comprising the vector, a protein chip comprising the polypeptides and a
 CC record comprising all or part of the data, listed in the specification.
 CC The complex, polypeptides, polynucleotides and compounds are useful for
 CC preventing or treating metabolic disorders such as obesity or diabetes.
 CC The polynucleotides are useful as probes or primers. The complex is
 CC particularly useful for identifying selected interacting domains (SID
 CC (RTM)) for screening drugs that modulate the protein interaction, thus
 CC exhibiting the therapeutic effect. The present sequence represents a SID
 CC (prey) protein of the invention
 XX
 SQ Sequence 766 AA;
 Query Match 46.1%; Score 541.5; DB 6; Length 766;
 Best Local Similarity 47.0%; Pred. No. 4.5e-53;
 Matches 103; Conservative 37; Mismatches 78; Indels 1; Gaps 1;
 QY 1 QNRKNRYRDIPLDYSTRVPLGKNKDYINASVIRVNEHEEYFYIATQGPLPETTEDFWQ 60
 DB 517 ENRKNRYKNILPYDATRVPLGEGYINASIKIPVGKEEFYIACQGPLTTVGDFFWQ 576

Qy	61	MYLENNCNVMIATREIECGVIKYSYWPISL-KEPLEBEHFSVFLETFHTHTVYTFVRVF	119
Db	577	MIWEQKSTVIAMWTQVEGEKIKQRYWPNILGKTTWVSNRLRLALVRMQLKGFVVRAM	636
Qy	120	QIVKSTGSKQCXKHLQFTKWPDDHGTASADFFIKYIVRYVKSHITGPILLVHCSAGVGR	179
Db	637	TLEDIQTREVRHISHLNFTAPDHDTPSQPDLLTFSYMRHHRSGFIITHCASAGIRS	696
Qy	180	GVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMQITK	218
Db	697	GTLICIDVVLGISODLPDIDSLVRCMRLQRHGMVQTE	735

RESULT 15

RESUL 13
AAG67637
ID AAG67637 standard; protein; 1267 AA.

AAG67637:

XX
DT 26-NOV-2001 (first entry)XX
DE Amino acid sequence of a human protein.

XX
Human: protein kinase: protein phosphatase: signal transduction.

OS Homo sapiens.

AA PN WO200109316-A1.

XX 08-FEB-2001.

XX
PF 28-JUL-2000: 2000WO-JP005061.

29-III-1999. 99,TP-00248036.

PR 18-OCT-1999; 99US-0159390E;
PR 11-JAN-2000; 2000JB-00118776

PR 17-FEB-2000; 2000US-01833322P.
PR 03 MAY 2000; 2000JP-00193767

PR 09-JUN-2000; 2000JP-00241899.

PA (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa

PI Senoo C, Nezu J;

DR WPI; 2001-570286/64.

PT New genes encoding

XX
PI activity, use ofps Example 4; Page 206-
vv

The specification describes human protein kinase/protein phosphatase gene participants. It is expected that the protein kinase/protein phosphatase gene participants in signal transduction in cells. The protein kinase/protein phosphatase polypeptides and polynucleotides are useful for developing diagnostics and treatment agents for human and animal diseases. The protein kinase/protein phosphatase polypeptides are useful as target molecules in designing novel drugs. The protein kinase/protein phosphatase polynucleotides are useful as a source of probes and primers, which may be used to isolate homologous sequences. The present sequence represents a human protein, which is used in the course of the invention.

Sequence 1267 AA:

Query Match	46.11%	Score 541.5;	DB 4;	Length 1267;
Best Local Similarity	47.0%;	Pred. No. 9.2e-53;		
Matches 103:	Conservative 37;	Mismatches 78;		
	Indels 1;	Gaps 1;		

QY 1 QNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDWQ 60
1018 ENRRKNRYKNILPYDSTRVPLGDEGYINASFIKIPVGKEEFVYIACQGFETTVGDFWQ 1077
Db

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OM protein - protein search, using sw model

Run on: December 1, 2004, 12:07:39 ; Search time 85.8421 Seconds
(without alignments)
1561.731 Million cell updates/sec

Title: US-09-095-478A-6_COPY_225_457

Perfect score: 1253

Sequence: 1 QNRDKNRYRDILPYDSTRVP.....MIQTKQYQFCYEVILEVLQ 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1253	100.0	426	2	O55082 mus musculus
2	995	79.4	398	2	Q9Y406 Q9Y406 homo sapien
3	607.5	48.5	2484	2	Q28006 bos taurus
4	598.5	47.8	2453	1	PTND MOUSE
5	595.5	47.5	2500	2	Q6EHH9 Q6EHH9 xenopus lae
6	592.5	47.3	2485	1	PTND HUMAN
7	510	40.7	920	2	Q6GPK7 Q6GPK7 xenopus lae
8	500	39.9	292	2	Q8N4S3 Q8N4S3 homo sapien
9	499	39.8	913	1	PTN3_HUMAN
10	493.5	39.4	926	2	Q9WU22 Q9WU22 mus musculus
11	488.5	39.0	1948	1	PTNS_HUMAN
12	486.5	38.8	2051	2	O44328 O44328 hirudo medi
13	485.5	38.7	468	2	Q9IBA0 Q9IBA0 potamotrygo
14	485.5	38.7	615	2	Q9IAI8 Q9IAI8 xenopus lae
15	484.5	38.7	468	2	Q9IBR2 Q9IBR2 potamotrygo
16	483.5	38.6	1502	2	Q9UM81 Q9UM81 homo sapien
17	482.5	38.5	749	2	Q8R169 Q8R169 mus musculus
18	482.5	38.5	857	2	Q90VJ4 Q90VJ4 brachydanio
19	482.5	38.5	1254	2	Q8VBV0 Q8VBV0 mus musculus
20	480.5	38.3	468	2	Q9NLO6 Q9NLO6 eptatretus
21	480.5	38.3	1222	2	Q8MY44 Q8MY44 eptatretus
22	479.5	38.3	1100	2	Q8MY45 Q8MY45 eptatretus
23	479.5	38.3	1187	2	Q8MY42 Q8MY42 eptatretus
24	479.5	38.3	1202	2	Q8MY43 Q8MY43 eptatretus
25	477.5	38.1	1896	2	Q9IAJ1 Q9IAJ1 xenopus lae
26	476.5	38.0	926	1	PTN4_HUMAN
27	475.5	37.9	907	2	Q8MY41 Q8MY41 eptatretus
28	475	37.9	1337	1	PTPJ_HUMAN
29	474.5	37.9	1501	2	Q7TT17 Q7TT17 mus musculus
30	474.5	37.9	1501	2	Q9QW00 Q9QW00 rattus sp.
31	474.5	37.9	1863	2	Q64605 Q64605 rattus norv

32	474.5	37.9	1904	2	Q64699 Q64699 mus musculus
33	474.5	37.9	1912	1	PTPD_HUMAN
34	473.5	37.8	469	2	Q9NL08 Q9NL08 eptatretus
35	473.5	37.8	1998	2	Q8CIW2 Q8CIW2 mus musculus
36	472.5	37.7	929	2	Q6NRP9 Q6NRP9 xenopus lae
37	472.5	37.7	929	2	Q6DCH9 Q6DCH9 xenopus lae
38	472.5	37.7	929	2	AAH70687 AAH70687 xenopus l
39	471.5	37.6	469	2	Q9NL11 Q9NL11 brachiosteo
40	471.5	37.6	1102	2	Q8OVN7 Q8OVN7 mus musculus
41	471	37.6	1238	2	Q8K3Q2 Q8K3Q2 mus musculus
42	471	37.6	1499	2	Q90815 Q90815 gallus gall
43	470.5	37.5	579	2	Q9JJ07 Q9JJ07 mus musculus
44	470	37.5	694	2	Q6DE20 Q6DE20 xenopus lae
45	469.5	37.5	1956	2	Q6MZf6 Q6MZf6 homo sapien

ALIGNMENTS

RESULT 1

OS5082					
ID	OS5082	PRELIMINARY;	PRT;	426	AA.
AC	OS5082;				
DT	01-JUN-1998	(Tremblrel. 06, Created)			
DT	01-JUN-1998	(Tremblrel. 06, Last sequence update)			
DT	01-OCT-2004	(Tremblrel. 28, Last annotation update)			
DE	Protein-tyrosine-phosphatase (EC 3.1.3.48) (Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4921505B14)				
DE	product:protein tyrosine phosphatase, non-receptor type 20, full insert sequence).				
GN	Name=Ptpn20;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Malattia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Testis;				
RX	MEDLINE=98070510; PubMed=9407093;				
RA	Ohsugi M., Kuramochi S., Matsuda S., Yamamoto T.;				
RT	"Molecular cloning and characterization of a novel cytoplasmic protein-tyrosine phosphatase that is specifically expressed in spermatocytes.";				
RL	J. Biol. Chem. 272:33092-33099(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Testis;				
RX	MEDLINE=99279253; PubMed=10349636;				
RA	Carninci P., Hayashizaki Y.;				
RT	"High-efficiency full-length cDNA cloning.";				
RL	Meth. Enzymol. 303:19-44(1999).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Testis;				
RX	MEDLINE=21085660; PubMed=11217851;				
RA	RIKEN FANTOM Consortium;				
RT	"Functional annotation of a full-length mouse cDNA collection.";				
RL	Nature 409:685-690(2001).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Testis;				
RA	The FANTOM Consortium,				
RT	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";				
RL	Nature 420:563-573(2002).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Testis;				
RX	MEDLINE=20499374; PubMed=11042159;				
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;				
RT	"Normalization and subtraction of cap-trapper-selected cDNAs to				

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RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[6]
RN
RP
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[7]
RN
RP
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; D64141; BAA23761.1; -.
DR EMBL; AK029493; BAC26476.1; -.
DR HSP; P10586; ILAR.
DR MGP; MGI:1196295; Ppnp20.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPc; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
DR KW Hydrolase; Receptor.
SQ
Query Match 426 AA; 49118 MW; 2B35PB13379502P4 CRC64;
Best Local Similarity 100.0%; Score 1253; DB 2; Length 426;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNRDKRYRDLIPYDSTVPLGKNKDYINASYIRIVNHEEYFYIATQGLPETIEDFWQ 60
DB 198 QNRDKRYRDLIPYDSTVPLGKNKDYINASYIRIVNHEEYFYIATQGLPETIEDFWQ 247
QY 61 MVLNNCNVIAITREIECGVIKCYSWPISLKEPLEFHFPSVLETFHTVQYFTVRVFQ 120
DB 248 MVLNNCNVIAITREIECGVIKCYSWPISLKEPLEFHFPSVLETFHTVQYFTVRVFQ 307
QY 121 IVKSTGSKQCCKHLQFTKWDHGTGPASADFFIKVYVRKSHITGPIIVHCSAGVGTG 180
DB 308 IVKSTGSKQCCKHLQFTKWDHGTGPASADFFIKVYVRKSHITGPIIVHCSAGVGTG 367
QY 181 VFICVDVVFSALEKNYSFDIMNIVTQMRKQRCMIQTKEQYQFCYEIVLEVLQ 233
DB 368 VFICVDVVFSALEKNYSFDIMNIVTQMRKQRCMIQTKEQYQFCYEIVLEVLQ 420

RESULT 2
QY406

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ID QY406 PRELIMINARY; PRT; 398 AA.
AC QY406;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein DKFZp566K0524 (Fragment).
GN Name=DKFZp566K0524;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP
RC TISSUE=Kidney;
RA Ansoerge W., Winkner U., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050040; CAB43248.1; -.
DR PIR; T08716; T08716.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPc; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
DR KW Hydrolase; Hypothetical protein.
FT NON TER
SQ
Query Match 398 AA; 45690 MW; 857AAD03747870A2 CRC64;
Best Local Similarity 79.4%; Score 995; DB 2; Length 398;
Matches 181; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

QY 2 NRDKRYRDLIPYDSTVPLGKNKDYINASYIRIVNHEEYFYIATQGLPETIEDFWQ 61
DB 161 NRDKRYRDLIPYDSTVPLGKNKDYINASYIRIVNHEEYFYIATQGLPETIEDFWQ 220
QY 62 VLENNCNVIAITREIECGVIKCYSWPISLKEPLEFHFPSVLETFHTVQYFTVRVFQ 121
DB 221 VLENNCNVIAITREIECGVIKCYSWPISLKEPLEFHFPSVLETFHTVQYFTVRVFQ 280
QY 122 VKKSTGSKQCCKHLQFTKWDHGTGPASADFFIKVYVRKSHITGPIIVHCSAGVGTG 181
DB 281 VEKSTGSHSVKQLQFTKWDHGTGPASADFFIKVYVRKSHITGPIIVHCSAGVGTG 340
QY 182 FICVDVVFSALEKNYSFDIMNIVTQMRKQRCMIQTKEQYQFCYEIVLEVLQ 233
DB 341 FLCVDVVFCAIVKDCSFNIMDIVAQMREQRSQSGVQTKHQYHFCYDIVLEVL 392

RESULT 3
QY406 PRELIMINARY; PRT; 2484 AA.
AC QY406;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE BA14.
OS Bos taurus (Bovine)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP
RC TISSUE=Testis;
RA Vega Q.C., Walton K.M., Dixon J.E.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 5 PDZ/DHR domains.
DR EMBL; U20807; AAA73516.1; -.

```


PDB; 1OZI; NMR; A=1351-1444.
 DR MGD; MGI:103293; Ptpn13.
 DR InterPro; IPR000299; Band 4.1.
 DR InterPro; IPR0009065; FERM.
 DR InterPro; IPR001478; PDZ.
 DR InterPro; IPR000387; TYR phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00373; Band_41; 1.
 DR Pfam; PF00595; PDZ; 5.
 DR Pfam; PF00102; Y phosphatase; 1.
 DR PRINTS; PR00935; BAND41.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00295; B41; 1.
 DR SMART; SM00228; PDZ; 5.
 DR SMART; SM00194; PTPC; 1.
 DR SMART; SM00404; PTPC motif; 1.
 DR PROSITE; PS00660; FERM_1; FALSE_NEG.
 DR PROSITE; PS00661; FERM_2; FALSE_NEG.
 DR PROSITE; PS00057; FERM_3; 1.
 DR PROSITE; PS0106; PDZ; 5.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS00056; TYR_PHOSPHATASE_PTP; 1.
 DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
 KW 3D-structure; Coiled Coil; Cytoskeleton; Hydrolase;
 KW Protein phosphatase; Repeat; Structural protein.
 FT DOMAIN 458 493 Coiled coil (Potential).
 FT DOMAIN 555 865 FERM.
 FT DOMAIN 1084 1170 PDZ 1.
 FT DOMAIN 1357 1442 PDZ 2.
 FT DOMAIN 1491 1579 PDZ 3.
 FT DOMAIN 1764 1845 PDZ 4.
 FT DOMAIN 1857 1942 PDZ 5.
 FT DOMAIN 2180 2434 Protein-tyrosine phosphatase.
 FT ACT_SITE 2375 Phosphotyrosine intermediate (By similarity).
 FT DOMAIN 56 59 Poly-Leu.
 FT CONFLICT 79 81 STA -> FTG (in Ref. 2).
 FT CONFLICT 156 168 HIRSNCAPSFN -> TSGTASRAFSY (in Ref. 2).
 V -> L (in Ref. 2).
 N -> I (in Ref. 2).
 K -> E (in Ref. 2).
 Q -> K (in Ref. 2).
 S -> L (in Ref. 2).
 S -> T (in Ref. 2).
 R -> Q (in Ref. 2).
 QTPHVQDYSPVTEENT -> KHPMSKTTALLLKII (in Ref. 1).
 D -> H (in Ref. 2).
 S -> P (in Ref. 1).
 N -> I (in Ref. 3).
 D -> N (in Ref. 2).
 S -> T (in Ref. 2).
 PGLPO -> GSHDAEQPKAPP (in Ref. 1).
 PGLPO -> 53396F27AE2582F2 CRC64;
 Query Match 47.8%; Score 598.5; DB 1; Length 2453;
 Best Local Similarity 50.0%; Pred. No. 2.6e-48;
 Matches 118; Conservative 37; Mismatches 74; Indels 7; Gaps 3;
 QY 1 QNRDKRYRDILPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
 DB 2203 ENRRKNRYKNILPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 2262
 QY 61 MVLENNCNVIAMITREIECGVICYSWPISL-KEPFEHFSVLETFHVTQYVF 119
 DB 2263 MVWEQNSVIAMTQVEGEKICQRYWPSILGTTTANERLRLALLRMOQLKGFIVRM 2322
 QY 120 QIVKSTGKSCQVHLQTKPDHGTTPASAD---EFIKVVRVVRKSHITGPLLHVCAGV 176
 DB 2323 ALEDIQTEVRHISHLNFTWPDHPTPSQFDLLTFISYMRHRS---GPTVTHCSAGI 2379
 QY 177 GRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMITQKEQYQFCYVILEVL 232
 DB 2380 GRSGLTICIDVVLGLISQLEFIDSLVRCMLQRHGMVQTEGQYFCYQVILDYL 2435

DB 2380 GRSGLTICIDVVLGLISQLEFIDSLVRCMLQRHGMVQTEGQYFCYQVILDYL 2435

RESULT 5
 Q6EHH9 PRELIMINARY; PRT; 2500 AA.
 AC Q6EHH9;
 DT 01-OCT-2004 (TrEMBLrel. 28, Created)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Frizzled-8 associated multidomain protein (Fragment).
 GN Name=FRIED;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lisovsky M.Y., Itoh K., Sokol S.Y.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RE EMBL; AY327257; AA97566.1; -
 FT NON_TER 2500 2500
 SQ SEQUENCE 2500 AA; 277694 MW; DDD27366EA19CA0 CRC64;
 Query Match 47.5%; Score 595.5; DB 2; Length 2500;
 Best Local Similarity 47.0%; Pred. No. 5.2e-48;
 Matches 111; Conservative 48; Mismatches 72; Indels 5; Gaps 2;
 QY 1 QNRDKRYRDILPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
 DB 2257 ENKKRYKNILPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 2316
 QY 61 MVLENNCNVIAMITREIECGVICYSWPISLKEPFEHFSVLETFHVTQY---FTVR 117
 DB 2317 MVWEQNSVIAMTQVEGEKICQRYWPSILGTTTANERLRLALLRMOQLKGFIVRM 2374
 QY 118 VFQIVKSTGKSCQVHLQTKPDHGTTPASADFFIKVVRVVRKSHITGPLLHVCAGV 177
 DB 2375 VLELHDITQSEVROIAHLNFTWPDHPTPSQFDLLTFISYMRHISGPIITHCSAGI 2434
 QY 178 RTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMITQKEQYQFCYVILEVLQ 233
 DB 2435 RSGTLICIDVLMALISKDLFPDISNMVHTWRQLRSHGMITQTEQYIFCYQVILYLK 2490

RESULT 6
 PTND HUMAN
 ID PTND HUMAN STANDARD; PRT; 2485 AA.
 AC Q12923; Q15159; Q15263; Q15264; Q15265; Q15674; Q16826; Q81WH7;
 AC Q9NYN9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Protein tyrosine phosphatase, non-receptor type 13 (EC 3.1.3.48)
 DE (Protein-tyrosine phosphatase 1E) (PTP-E1) (hPTPE1) (PTP-BAS)
 DE (Protein-tyrosine phosphatase PTP1L) (Fas-associated protein-tyrosine phosphatase 1) (FAP-1)
 DE Name=PTPN13; Synonyms=PTP1E, PTP1L, PNP1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 4).
 RC TISSUE=Breast carcinoma;
 RX MEDLINE=94350988; PubMed=8071359;
 RA Banville D., Ahmad S., Stocco R., Shen S.-H.;
 RA "A novel protein-tyrosine phosphatase with homology to both the cytoskeletal proteins of the band 4.1 family and junction-associated guanylate kinases".
 RT J. Biol. Chem. 269:22320-22327(1994).
 RL

RN [2]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Leukemia;
 RX MEDLINE=94116679; PubMed=8287977;
 RA Maekawa K., Imagawa N., Nagamatsu M., Harada S.;
 RT "Molecular cloning of a novel protein-tyrosine phosphatase containing
 RL a membrane-binding domain and GUG repeats.";
 RL FEBS Lett. 337:200-206(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95014139; PubMed=7929060;
 RA Saras J., Claesson-Welsh L., Heldin C.-H., Gonez L.J.;
 RT "cloning and characterization of PTP11, a protein tyrosine phosphatase
 RL with similarities to cytoskeletal-associated proteins.";
 RL J. Biol. Chem. 269:24082-24089(1994).
 RN [4]
 RP SEQUENCE OF 1216-2490 FROM N.A.
 RC TISSUE=Pancreas;
 RX Wang H.Y.;
 RA Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 1279-1883 FROM N.A. (ISOFORM 4).
 RC TISSUE=Brain;
 RX MEDLINE=95232528; PubMed=7536343;
 RA Sato T., Irie S., Kitada S., Reed J.C.;
 RT "FAP-1: a protein tyrosine phosphatase that associates with Fas.";
 RL Science 268:411-415(1995).
 RN [6]
 RP SEQUENCE OF 1323-1821 FROM N.A.
 RA Irie S., Hachiya T., Sato T.A.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 1323-1922 FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP INTERACTION WITH TRIP6.
 RX MEDLINE=99329089; PubMed=10400701;
 RA Murthy K.K., Clark K., Fortin Y., Shen S.-H., Banville D.;
 RT "TRP-1, a zyxin-related protein, interacts with the second PDZ domain
 RL of the cytosolic protein tyrosine phosphatase hPTP1E.";
 RL J. Biol. Chem. 274:20679-20687(1999).
 RN [9]
 RP INTERACTION WITH NGFR.
 RX MEDLINE=20012928; PubMed=10544233;
 RA Irie S., Hachiya T., Rabizadeh S., Maruyama W., Mukai J., Li Y.,
 RA Reed J.C., Bredesen D.E., Sato T.A.;
 RT "Functional interaction of Fas-associated phosphatase-1 (FAP-1) with
 RL p75(NTR) and their effect on NF-kappaB activation.";
 RL FEBS Lett. 460:191-198(1999).
 RN [10]
 RP INTERACTION WITH PLEKHA1 AND PLEKHA2.
 RX PubMed=14516276; DOI=10.1042/BJ20031154;
 RA Kimber W.A., Deak M., Prescott A.R., Alessi D.R.;
 RT "Interaction of the protein tyrosine phosphatase PTP11 with the
 RL PtdIns(3,4)P2-binding adaptor protein TAPP1.";
 RL Biochem. J. 376:525-535(2003).
 RN [11]
 RP STRUCTURE BY NMR OF 1361-1456 UNCOMPLEXED AND IN COMPLEX WITH THE
 RP C-TERMINUS OF TNFRSF6.
 RX MEDLINE=20170882; PubMed=10704206;
 RA Kozlov G., Gehring K., Ekiel I.;
 RT "Solution structure of the PDZ2 domain from human phosphatase hPTP1E
 RL and its interactions with C-terminal peptides from the Fas receptor.";
 RL Biochemistry 39:2572-2580(2000).
 RN [12]
 RP STRUCTURE BY NMR OF 1361-1456 IN COMPLEX WITH THE C-TERMINUS OF THE
 RP GUANINE NUCLEOTIDE EXCHANGE FACTOR RA-GEF-2.
 RX MEDLINE=22090786; PubMed=12095257; DOI=10.1016/S0022-2836(02)00544-2;
 RA Kozlov G., Banville D., Gehring K., Ekiel I.;
 RT "Solution structure of the PDZ2 domain from cytosolic human
 RL phosphatase hPTP1E complexed with a peptide reveals contribution of
 RL the beta2-beta3 loop to PDZ domain-ligand interactions.";
 RL J. Mol. Biol. 320:813-820(2002).
 RN [13]
 RP VARIANTS PRO-1419 AND MET-1522.
 RX MEDLINE=22323362; PubMed=12436199; DOI=10.1007/s100380200094;
 RA Yoshida S., Harada H., Nagai H., Fukino K., Teramoto A., Emi M.;
 RT "Head-to-head juxtaposition of Fas-associated phosphatase-1 (FAP-1)
 RL and c-Jun NH2-terminal kinase 3 (JNK3) genes: genomic structure and
 RL seven polymorphisms of the FAP-1 gene.";
 RL J. Hum. Genet. 47:614-619(2002).
 CC -I- FUNCTION: Regulates negatively Fas-induced apoptosis and NGFR-
 CC mediated pro-apoptotic signaling.
 CC -I- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -I- SUBUNIT: Interacts with TRIP6 and TNFRSF6 (Fas receptor) through
 CC its second PDZ domain. Interacts with the C-terminal SVP motif of
 CC NGFR through its third PDZ domain. Interacts with the LIM domain
 CC of PDLIM4 through its second and fourth PDZ domains. Binds PLEKHA1
 CC and PLEKHA2 through its first PDZ domain.
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1;
 CC IsoId=Q12923-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q12923-2; Sequence=VSP_000496;
 CC Name=3;
 CC IsoId=Q12923-3; Sequence=VSP_000497;
 CC Name=4;
 CC IsoId=Q12923-4; Sequence=VSP_007921;
 CC Note=May be due to a competing donor splice site;
 CC -I- TISSUE SPECIFICITY: Present in most tissues with the exception of
 CC the liver and skeletal muscle. Most abundant in lung, kidney and
 CC fetal brain.
 CC -I- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Non-receptor class subfamily.
 CC -I- SIMILARITY: Contains 1 FERM domain.
 CC -I- SIMILARITY: Contains 5 PDZ/DHR domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U12128; AAB60339.1; -
 DR EMBL; D21209; BAA04750.1; -
 DR EMBL; D21210; BAA04751.1; -
 DR EMBL; D21211; BAA04752.1; -
 DR EMBL; X80289; CAA56563.1; -
 DR EMBL; X79676; CAA56124.1; -

DR	EMBL; L34583; AAC41755.1; ..	RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
DR	EMBL; AF233233; AAF63474.1; ..	RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
DR	EMBL; BC039610; AAH39610.1; ALT_TERM.	RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
DR	PIR; A54971; A54971.	RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
DR	PIR; I67629; I67629.	RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
DR	PIR; I67630; I67630.	RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
DR	PDB; 1DSG; NMR; A=1361-1456.	RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
DR	PDB; 1Q7X; NMR; A=1357-1459.	RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
DR	PDB; 3PDZ; NMR; A=1361-1456.	RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
DR	Genew; HGNC:9646; PTPN13.	RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
DR	MM; 600267; ..	RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
DR	GO; GO:0004725; F-protein-tyrosine-phosphatase activity; TAS.	RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
DR	GO; GO:006470; P-protein amino acid dephosphorylation; TAS.	RT	Johnson S.J., Marra M.A.;
DR	InterPro; IPR000299; Band 4.1.	RT	"Generation and initial analysis of more than 15,000 full-length human
DR	InterPro; IPR009065; FERM.	RT	and mouse cDNA sequences";
DR	InterPro; IPR011009; Kinase_like.	RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
DR	InterPro; IPR001478; PDZ.	RN	[2]
DR	InterPro; IPR011036; PH related.	RN	SEQUENCE FROM N.A.
DR	InterPro; IPR000387; TYR_phosphatase.	RC	TISSUE=Oocytes;
DR	InterPro; IPR000242; Tyr_PP.	RC	MEDLINE=22341132; PubMed=12454917;
DR	Pfam; PF00373; Band 41; 1.	RX	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
DR	Pfam; PF00595; PDZ; 5.	RA	Richardson P.;
DR	PRINTS; PR00935; BAND41.	RA	"Genetic and genomic tools for Xenopus research: The NIH Xenopus
DR	PRINTS; PR00700; PRTPHPTASE.	RT	initiative";
DR	PROSITE; PS00660; FERM_1; FALSE_NEG.	RL	Dev. Dyn. 225:384-391(2002).
DR	PROSITE; PS00661; FERM_2; FALSE_NEG.	RN	[3]
DR	PROSITE; PS00057; FERM_3; 1.	RC	SEQUENCE FROM N.A.
DR	PROSITE; PS0106; PDZ; 5.	RC	TISSUE=Oocytes;
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.	RA	Klein S., Strausberg R.;
DR		RA	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR		CC	-1- SIMILARITY: Contains 1 PDZ/DHR domain.
DR		DR	EMBL; BC073110; AAH73110.1; ..
DR		DR	InterPro; IPR000299; Band 4.1.
DR		DR	InterPro; IPR000798; Ez/rad/moesin.
DR		DR	InterPro; IPR009065; FERM.
DR		DR	InterPro; IPR001478; PDZ.
DR		DR	InterPro; IPR011036; PH related.
DR		DR	InterPro; IPR003595; PTPC motif.
DR		DR	InterPro; IPR000387; TYR_phosphatase.
DR		DR	InterPro; IPR000242; Tyr_PP.
DR		DR	Pfam; PF00373; Band 41; 1.
DR		DR	Pfam; PF00595; PDZ; 1.
DR		DR	Pfam; PF00102; Y_phosphatase; 1.
DR		DR	PRINTS; PR00935; BAND41.
DR		DR	PRINTS; PR00661; ERM FAMILY.
DR		DR	PRINTS; PR00700; PRTPHPTASE.
DR		DR	SMART; SM00295; B41; 1.
DR		DR	SMART; SM00228; PDZ; 1.
DR		DR	SMART; SM00194; PTPC; 1.
DR		DR	SMART; SM00404; PTPC motif; 1.
DR		DR	PROSITE; PS00660; FERM_1; UNKNOWN_1.
DR		DR	PROSITE; PS00057; FERM_3; 1.
DR		DR	PROSITE; PS0106; PDZ; 1.
DR		DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR		DR	PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR		DR	PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW			Hydrolase; Hypothetical protein.
SQ			SEQUENCE 920 AA; 105109 MW; 8F0BB89C359CD41E CRC64;
			Query Match 40.7%; Score 510; DB 2; Length 920;
			Best Local Similarity 43.5%; Pred. No. 2.9e-40;
			Matches 104; Conservative 33; Mismatches 88; Indels 14; Gaps 4;
Qy	1 QNRDKRYRDLIPYDSTRVPLGKKNKYINASYI-----RIVNHEBEYFYATQGPLPE 53		
Db	676 QNMDRNYKQVLPYDSTRVPLGKKNKYINASYI-----RIVNHEBEYFYATQGPLPE 730		
Qy	54 TIEDFWQVLENNCNVAMITREICGVKCYWPISLKEPLEFEHFSVLETFHVTQY 113		
Db	731 TCAQFWQVLENNCNVAMITREICGVKCYWPISLKEPLEFEHFSVLETFHVTQY 789		
Qy	114 FTVRVFQIVKXSTGSKQCVKHLQTKPDPHGTPASADFFIKVVRVVRKSHITG-PLLVHC 172		

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Db 790 YVREMLLTDTTETGDEFFIIHLOQYVAMPDHGVPDDSSDFLEFATYVRQKEMENQPVLVHC 849
QY 173 SAGVGRGTGVCVDDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOQKEQYQFCYEVILEV 231
Db 850 SAGIGRTGLVITMETANCLIEHQNPVPLDVVRQMRDQRAMVQTSQYKFKVCEAILRV 908

RESULT 8
QBN4S3
ID QBN4S3 PRELIMINARY; PRT; 292 AA.
AC QBN4S3;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Kidney;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033716; AAH33716.1; -.
DR GO; GO:0016787; F-hydrolase activity; IEA.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase; Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 292 AA; 33121 MW; 548388BDD41D1BD7 CRC64;

Query Match 39.9%; Score 500; DB 2; Length 292;
Best Local Similarity 42.0%; Pred. No. 6 Se-40;
Matches 102; Conservative 38; Mismatches 85; Indels 18; Gaps 5;

QY 1 QNRDKNRYDILPYDSTRVPLGKXKYNYSYI-----RIVNHEEYFYIATQGPLPE 53
Db 48 QNLDKNRYKDLVPTDTRVLQGNEDYINASYVMEIPAAVLNK-----YIATQGPLPH 102
QY 54 TIEDFMQVLENNCNVITAMITRIECCGVIKCYVWPISLKEPLEFEH--PSVLETFHVT 111
Db 103 TCAQFQVQVVDQKLSLIVMLTTITERGTRKCHQWTP---DPPDMNHGGPHIOCSSEDT 159
QY 112 QYFTVFVFQVVKKSTGKSCQVHQLQFQKPDHGTGPASADFFIKYRVYRKSHI--TGPLLV 170
Db 160 IAVSREMLVNTQTGEHTVTHLQYVAMPDHGVPDDSSDFLEFVNVVRSILRVDSEPLV 219
QY 171 HCSAGVGRGTGVCVDDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOQKEQYQFCYEVILE 230
Db 220 HCSAGIGRTGLVITMETANCLIEHQNPVPLDVVRQMRDQRAMVQTSQYKFKVCEAILR 279
QY 231 VLQ 233
Db 280 VYE 282

RESULT 9
PTN3_HUMAN
ID PTN3_HUMAN STANDARD; PRT; 913 AA.
AC P26045;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 3 (EC 3.1.3.48)
```

```
DE (Protein-tyrosine phosphatase H1) (PTP-H1).
GN Name=PTPN3; Synonyms=PTPH1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91296738; PubMed=1648725;
RA Yang Q., Tonks N.K.;
RT "Isolation of a cDNA clone encoding a human protein-tyrosine
RT phosphatase with homology to the cytoskeletal-associated proteins band
RT 4.1, ezrin, and talin.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5949-5953 (1991).
RN [2]
RP SEQUENCE OF 194-896 FROM N.A.
RC Tissue=Colon;
RX MEDLINE=92327504; PubMed=1626183;
RA Arimura Y., Hinoda Y., Itoh F., Takekawa M., Tsujisaki M., Adachi M.,
RA Imai K., Yachi A.;
RT "cDNA cloning of new protein tyrosine phosphatases in the human
RT colon.";
RL Tumour Biol. 13:180-186 (1992).
RN [3]
RP SEQUENCE OF 899-913 FROM N.A.
RX MEDLINE=95179278; PubMed=7874267;
RA Ikuta S., Itoh F., Hanoda Y., Toyota M., Makiguchi Y., Imai K.,
RA Yachi A.;
RT "Expression of cytoskeletal-associated protein tyrosine phosphatase
RT PTPH1 mRNA in human hepatocellular carcinoma.";
RL J. Gastroenterol. 29:727-732 (1994).
CC -!- FUNCTION: May act at junctions between the membrane and the
CC cytoskeleton.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -!- SIMILARITY: Contains 1 FERM domain.
CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC
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CC
CC -----
CC EMBL; M64572; AAA35647.1; -.
CC EMBL; S39392; AAB22439.2; -.
CC EMBL; S76309; AAB33583.1; -.
CC PIR; A41109; A41109.
CC HSSP; P18031; 1C88.
CC Genew; HGNC:9655; PTPN3.
CC MTM; 176877; -.
CC GO; GO:0004725; P:protein-tyrosine-phosphatase activity; TAS.
CC GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
CC InterPro; IPR000299; Band 4.1.
CC InterPro; IPR000798; Ez/rad/moesin.
CC InterPro; IPR009065; FERM.
CC InterPro; IPR001478; PDZ.
CC InterPro; IPR011036; PH-related.
CC InterPro; IPR000387; TYR_phosphatase.
CC InterPro; IPR000242; Tyr_PP.
CC Pfam; PF00373; Band 41; 1.
CC Pfam; PF00595; PDZ_1.
CC Pfam; PF00102; Y_phosphatase; 1.
CC PRINTS; PR00935; BAND41.
CC PRINTS; PR00700; PRTYPHPTASE.
CC SMART; SM00295; B41; 1.
CC SMART; SM00228; PDZ; 1.
CC SMART; SM00194; PTPC; 1.
```

DR PROSITE; PS00660; FERM 1; 1.
DR PROSITE; PS00661; FERM 2; 1.
DR PROSITE; PS0057; FERM 3; 1.
DR PROSITE; PS00106; PDZ; 1.
DR PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
DR PROSITE; PS0056; TYR PHOSPHATASE 2; 1.
DR PROSITE; PS0055; TYR PHOSPHATASE_PTP; 1.
KW Cytoskeleton; Hydrolase; Protein phosphatase; Structural protein.
FT DOMAIN 29 312 FERM.
FT DOMAIN 510 582 PDZ.
FT DOMAIN 670 913 Protein-tyrosine phosphatase.
FT ACT_SITE 842 842 Phosphocysteine intermediate (By similarity).
SQ SEQUENCE 913 AA; 104029 MW; 29A539ACD2F1515 CRC64;

Query Match 39.8%; Score 499; DB 1; Length 913;
Best Local Similarity 42.0%; Pred. No. 3.3e-39;
Matches 102; Conservative 38; Mismatches 85; Indels 18; Gaps 5;

QY 1 QNRDKRYRDLIPYDSTRVPLGKNKDYINASYI-----RIVNHEEYFYIATQGPLPE 53
DB 669 QNRDKRYRDLIPYDSTRVPLGKNKDYINASYI-----RIVNHEEYFYIATQGPLPH 723

QY 54 TIEDFWQMLNENCNVIMITREIEGVIKCYWPISEKLEFEH--FSVLETFHVT 111
DB 724 TCAQFQVQVWDQKLSLIVMLTTLTERGRTKCHOYWP---DPPDVNHHGGPHIQCSQEDCT 780

QY 112 QYTVTRVFIQVKSTGKSCQVHLOFTKPDHGTPTASADFFIKYVYVR--KSHITGTL 170
DB 781 IAYVSREMLVTNTQTGEHTVTHLQYVAMPDHGIPDDSDFLFVNVYRSLRVDSEFVLV 840

QY 171 HCSAGVGTGVCVDFVFSIAEKNSYFDMIVTQMRKQRCGMIQTKEQYQFCYEIVL 230
DB 841 HCSAGIGRTGLVMTMETAMCLTERNLPYELDIVRKMQRDQAMVQSSQYKFCVCAILR 900

QY 231 VLQ 233
DB 901 VYE 903

RESULT 10

Q9MU22 PRELIMINARY; PRT; 926 AA.
AC Q9MU22;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Testis-enriched protein tyrosine phosphatase.
GN Name:Ptpn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=20510023; PubMed=11054567;
RA Park K.W., Lee E.J., Lee S.H., Lee J.E., Choi E.Y., Kim B.J.,
RA Hwang R., Park K.A., Baik J.H.;
RT "Molecular cloning and characterization of a protein tyrosine
RT phosphatase enriched in testis, a putative murine homologue of human
RT PTPMEG,"
RL Gene 257:45-55(2000).
RN [2]
RS SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Choi E.-Y., Park K.-W., Lee E.-J., Baik J.-H.;
RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 PDZ/DHR domain.
DR EMBL; AF106702; AAD22773.1; -.
DR HSSP; F11171; 1GG3.
DR MGD; MGI:1095792; Ptpn4.
DR GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. . . ; IDA.

DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR000798; Ez/rad/moesin.
DR InterPro; IPR009065; FERM.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR011036; PH related.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00373; Band 41; 1.
DR Pfam; PF00395; PDZ; 1.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00935; BAND41.
DR PRINTS; PR00661; ERMFAMILY.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00295; B41; 1.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00660; FERM 1; UNKNOWN_1.
DR PROSITE; PS00661; FERM 2; 1.
DR PROSITE; PS0057; FERM 3; 1.
DR PROSITE; PS0106; PDZ; 1.
DR PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
DR PROSITE; PS0056; TYR PHOSPHATASE 2; 1.
DR PROSITE; PS0055; TYR PHOSPHATASE_PTP; 1.
KW Hydrolase.
SQ SEQUENCE 926 AA; 105713 MW; A344DAD4FF7E2AE2 CRC64;

Query Match 39.4%; Score 493.5; DB 2; Length 926;
Best Local Similarity 41.2%; Pred. No. 1.1e-38;
Matches 101; Conservative 43; Mismatches 80; Indels 21; Gaps 5;

QY 1 QNRDKRYRDLIPYDSTRVPLGKNKDYINASYI-----IVNHEEYFYIATQGPLPE 53
DB 678 QNRDKRYRDLIPYDSTRVPLGKNKDYINASYI-----IVNHEEYFYIATQGPLPH 732

QY 54 TIEDFWQMLNENCNVIMITREIEGVIKCYWPISEKLEFEHFSVLETFHVTQ- 112
DB 733 TCKDFWQMIWEQSSMVVMLTTQVGRVKCHOYWP-----EPSESSYGCYQATCHEEG 788

QY 113 -YFTVRVFIQVKSTGKSCQVHLOFTKPDHGTPTASADFFIKYVYVR--KSHITGTL 168
DB 789 NPATIFRKTMLNQEKNESRQLTQIQTAWPDHGVDDSDFLDFVCHVDQAGKEEPI 848

QY 169 LVHCSAGVGTGVCVDFVFSIAEKNSYFDMIVTQMRKQRCGMIQTKEQYQFCYEIV 228
DB 849 IVHCSAGIGRTGLVMTMETAMCLTERNLPYELDIVRKMQRDQAMVQSSQYKFCVCEAI 908

QY 229 LEVLQ 233
DB 909 LKVE 913

RESULT 11

PTNS_HUMAN STANDARD; PRT; 1948 AA.
AC Q1332; O75255; O75870; Q15718; Q16341;
DT 10-OCT-2003 (Rel. 42, Created)
DT 01-OCT-2004 (Rel. 45, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Receptor-type protein-tyrosine phosphatase S precursor (EC 3.1.3.48)
DE (R-PTP-S) (Protein-tyrosine phosphatase sigma) (R-PTP-sigma).
GN Name:PTPRS;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Fetal brain.
RX MEDLINE=96102179; PubMed=8524829;
RA Pulido R., Serra-Pages C., Tang M., Streuli M.;
RT "The LAR/PTP delta/PTP sigma subfamily of transmembrane protein-
RT tyrosine-phosphatases: multiple human LAR, PTP delta, and PTP sigma
RT isoforms are expressed in a tissue-specific manner and associate with

RT the LAR-interacting protein LIP.1.1.;
 RL Proc. Natl. Acad. Sci. U.S.A. 92:111686-11690(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96225039; PubMed=8992885;
 RA Endo N., Rutledge S.J., Opas E.E., Vogel R., Rodan G.A., Schmidt A.;
 RT "Human protein tyrosine phosphatase-sigma: alternative splicing and
 RL inhibition by bisphosphonates.";
 RJ J. Bone Miner. Res. 11:535-543(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX PubMed=15057824; DOI=10.1038/nature02399;
 RA Grimwood J., Gordon L.A., Olsen A.S., Terry J., Schmutz J.,
 RL Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
 RA Azerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,
 RA Caenepeel S., Carrano A.V., Caillie C., Chan Y.M., Christensen M.,
 RA Cleland C., Copeland A., Dalin E., Dehal P., Denys M., Dettler J.C.,
 RA Escobar J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M.,
 RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,
 RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,
 RA Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,
 RA Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,
 RA Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,
 RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,
 RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
 RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,
 RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
 RA Furey T.S., DeLong P., Dickson M., Gordon D., Eichler E.E.,
 RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
 RA Rubin E.M., Lucas S.M.;
 RL "The DNA sequence and biology of human chromosome 19.";
 RN Nature 428:529-535(2004).
 RP SEQUENCE OF 1503-1589 FROM N.A.
 RX MEDLINE=92119637; PubMed=1370651;
 RA Adachi M., Sekiya A., Arimura Y., Takekawa M., Itch P., Hinoda Y.,
 RL Imai K., Yachi A.;
 RT "Protein-tyrosine phosphatase expression in pre-B cell NALM-6.";
 RJ Cancer Res. 52:737-740(1992).
 RN [5]
 RP INTERACTIONS WITH PP1A1; PP1A2 AND PP1A3.
 RX MEDLINE=98288299; PubMed=9624153;
 RA Serra-Pages C., Medley O.G., Tang M., Hart A., Streuli M.;
 RL "Liprins, a family of LAR transmembrane protein-tyrosine phosphatase-
 interacting proteins.";
 RJ J. Biol. Chem. 273:15611-15620(1998).
 CC -1- FUNCTION: Interacts with LAR-interacting protein LIP.1.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBUNIT: Interacts with PP1A1, PP1A2 and PP1A3.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;
 CC Comment=Additional isoforms seem to exist;
 CC Name=PTPS;
 CC IsoId=Q13332-1; Sequence=Displayed;
 CC Name=PTPS-NEA;
 CC IsoId=Q13332-2; Sequence=VSP_050021;
 CC Name=PTPS-MEB;
 CC IsoId=Q13332-3; Sequence=VSP_050022, VSP_050026, VSP_050027;
 CC Name=PTPS-MEC;
 CC IsoId=Q13332-4; Sequence=VSP_050024;
 CC Name=PTPS-P4-7;
 CC IsoId=Q13332-5; Sequence=VSP_050023, VSP_050025;
 CC -1- TISSUE SPECIFICITY: Detected in all tissues tested except for
 CC placenta and liver.
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Receptor class 2A subfamily.
 CC -1- SIMILARITY: Contains 8 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
 CC -----
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 CC -----
 DR EMBL; U5234; AAC50299.1; -;
 DR EMBL; U40317; AAC50567.1; -;
 DR EMBL; AC005790; AAC62832.1; -;
 DR EMBL; AC005338; AAC27825.1; -;
 DR EMBL; AC005788; AAC62834.1; -;
 DR EMBL; S78080; AAB21146.2; -;
 DR HSSP; P10586; ILAR.
 DR Genew; HGNC:9681; PTPRS.
 DR MIM; 601576; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.
 DR InterPro; IPR003962; FNIII subd.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig C2.
 DR InterPro; IPR000387; TYR phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00041; fn3; 8.
 DR Pfam; PF00047; Ig; 3.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PR00114; FNTYPEPHTASE.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00060; FN3; 8.
 DR SMART; SM00408; IGC2; 3.
 DR SMART; SM00194; PTPC; 2.
 DR PROSITE; PS50853; IG LIKE; 3.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS00055; TYR_PHOSPHATASE_FTP; 2.
 KW Alternative splicing; Cell adhesion; Glycoprotein; Hydrolase;
 KW Immunoglobulin domain; Protein phosphatase; Receptor; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 29 Potential.
 FT CHAIN 30 1948 Receptor-type protein-tyrosine
 FT DOMAIN 30 1282 phosphatase S. (Potential).
 FT TRANSMEM 1283 1303 Extracellular.
 FT DOMAIN 1304 1948 Potential.
 FT DOMAIN 135 123 Cytoplasmic (Potential).
 FT DOMAIN 135 233 Ig-like C2-type 1.
 FT DOMAIN 245 327 Ig-like C2-type 2.
 FT DOMAIN 332 420 Ig-like C2-type 3.
 FT DOMAIN 426 520 Fibronectin type-III 1.
 FT DOMAIN 525 614 Fibronectin type-III 2.
 FT DOMAIN 618 715 Fibronectin type-III 3.
 FT DOMAIN 720 828 Fibronectin type-III 4.
 FT DOMAIN 836 923 Fibronectin type-III 5.
 FT DOMAIN 928 1031 Fibronectin type-III 6.
 FT DOMAIN 1033 1117 Fibronectin type-III 7.
 FT DOMAIN 1393 1648 Fibronectin type-III 8.
 FT DOMAIN 1680 1930 Protein-tyrosine phosphatase 1.
 FT DOMAIN 641 644 Protein-tyrosine phosphatase 2.
 FT DISULFID 54 107 Poly-Pro.
 FT DISULFID 156 216 Potential.
 FT DISULFID 266 311 Potential.
 FT ACT_SITE 1589 1589 Phosphocysteine intermediate (By
 FT similarity).
 FT ACT_SITE 1880 1880 Phosphocysteine intermediate (By
 FT similarity).
 FT CARBOHYD 263 263 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 308 308 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 733 733 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 940 940 N-linked (GlcNAc. . .) (Potential).
 FT VARSPPLIC 190 198 Missing (in isoform PTPS-NEA).

```

FT VARSPLIC 236 239 /Ftlid-VSP 050021.
FT Missing (in isoform PTPS-MEB).
FT /Ftlid-VSP 050022.
FT VARSPLIC 617 1034 Missing (in isoform PTPS-F4-7).
FT /Ftlid-VSP 050023.
FT VARSPLIC 784 792 Missing (in isoform PTPS-MEC).
FT /Ftlid-VSP 050024.
FT VARSPLIC 1035 1035 V -> I (in isoform PTPS-F4-7).
FT /Ftlid-VSP 050025.
FT VARSPLIC 1350 1365 Missing (in isoform PTPS-MEB).
FT /Ftlid-VSP 050026.
FT VARSPLIC 1366 1366 S -> G (in isoform PTPS-MEB).
FT /Ftlid-VSP 050027.
FT CONFLICT 310 310 T -> HP (in Ref. 2).
FT CONFLICT 428 429 SA -> RP (in Ref. 2).
FT CONFLICT 742 745 RSPA -> LGPV (in Ref. 1).
FT CONFLICT 765 766 GA -> RR (in Ref. 2).
FT CONFLICT 768 768 A -> G (in Ref. 1).
FT CONFLICT 771 773 PPR -> RRS (in Ref. 2).
FT CONFLICT 910 910 R -> P (in Ref. 2).
FT CONFLICT 986 994 AAEFGAENA -> GRUSRRRT (in Ref. 2).
FT CONFLICT 995 995 L -> V (in Ref. 1).
FT CONFLICT 1195 1196 SL -> TV (in Ref. 1).
FT CONFLICT 1310 1313 Missing (in Ref. 3).
FT CONFLICT 1431 1431 S -> F (in Ref. 1).
FT CONFLICT 1457 1457 R -> C (in Ref. 3).
FT CONFLICT 1546 1546 E -> D (in Ref. 4).
FT CONFLICT 1587 1587 V -> A (in Ref. 4).
FT CONFLICT 1705 1705 N -> K (in Ref. 2).
FT SEQUENCE 1948 AA; 217093 MW; D3D211B18B3866DD CRC64;

Query Match 39.08; Score 488.5; DB 1; Length 1948;
Best Local Similarity 41.9%; Pred. No. 8.6e-38;
Matches 101; Conservative 45; Mismatches 80; Indels 15; Gaps 6;

QY 2 NRDKNRVDILPYDSTRVPLG-----KNDYINASYIRIVNHEEYFYIATQGPLPTIE 56
Db 1705 NKFNRLNVLPIYESTRVCLQPIRGVSDYINASFID--GYRQKAYIATQGLAETTE 1762
QY 57 DFWQWLENNCNVMIATREIECGVIKCYSWPISLKEPLEFHFSPV-LTFHVTQYFT 115
Db 1763 DFWRLWENNSTIVMLTKLREMGREKCHQWP--AERSARYQYFVVDPAEYNNPQYI- 1819
QY 116 VRVQIVKSTGKQCQVKHLOFTKWPDHGTGPASADFFIKYVYVRKSH-----ITGELLVH 171
Db 1820 LREFKVTARDGQSRTRQFQTDWPEQGVKSGEGFDFTGQVHKTKEQGQGPISVH 1879
QY 172 CSAGVGRGVFICVDVWFSAIEKNYSFDIMNIVTQMRKQRCGMIOTKEQYQCYEIVLEV 231
Db 1880 CSAGVGRGVFIVTILSVLERNRYEGVDFIQTVKMLRTQRPAMVQTEDEYQFCYQAALAY 1939
QY 232 L 232
Db 1940 L 1940

RESULT 12
O44328 PRELIMINARY; PRT; 2051 AA.
AC O44328;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-WAR-2004 (TREMBlrel. 26, Last annotation update)
DE Receptor tyrosine phosphatase.
GN Name=HmlAR2;
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98195364; PubMed=9526016;
RA Gerahon T.R., Baker M.W., Nitabach M., Wu P., Macagno E.R.;

RT "Two receptor tyrosine phosphatases of the IAR family are expressed in
RT the developing leech by specific central neurons as well as select
RT peripheral neurons, muscles, and other cells.";
RL J. Neurosci. 18:2991-3002 (1998).
DR EMBL; AF017083; AAB91460.1; -.
DR PIR; T30938; T30938.
DR HSSP; P10586; ILAR.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003962; FNIII_subd.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; fn3; 8.
DR Pfam; PF00047; ig; 2.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00014; ENTYPETIII.
DR PRINTS; PR00700; PRTPHPHTASE.
DR SMART; SM00060; FN3; 8.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS50853; FN3; 8.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase; Receptor.
SQ SEQUENCE 2051 AA; 229604 MW; D60F8A032F659B00 CRC64;

Query Match 38.88; Score 486.5; DB 2; Length 2051;
Best Local Similarity 41.1%; Pred. No. 1.4e-37;
Matches 99; Conservative 45; Mismatches 82; Indels 15; Gaps 6;

QY 2 NRDKNRVDILPYDSTRVPLG-----KNDYINASYIRIVNHEEYFYIATQGPLPTIE 56
Db 1808 NKQKRLNVLPIYESTRVCLQPIRGVSDYINASFID--GYRRAVYIATQGLPDTVE 1865
QY 57 DFWQWLENNCNVMIATREIECGVIKCYSWPISLKEPLEFHFSPV-LTFHVTQYFT 115
Db 1866 DFWRLWENNSTIVMLTKLREMGREKCHQWP--AERSARYQYFVVDPAEYNNPQYI- 1922
QY 116 VRVQIVKSTGKQCQVKHLOFTKWPDHGTGPASADFFIKYVYVRKSH-----ITGELLVH 171
Db 1923 LREFKVTARDGQSRTRQFQTDWPEQGVKSGEGFDFTGQVHKTKEQGQGPISVH 1982
QY 172 CSAGVGRGVFICVDVWFSAIEKNYSFDIMNIVTQMRKQRCGMIOTKEQYQCYEIVLEV 231
Db 1983 CSAGVGRGVFIVTILSVLERNRYEGVDFIQTVKMLRTQRPAMVQTEDEYQFCYQAALAY 2042
QY 232 L 232
Db 2043 L 2043

RESULT 13
Q91BA0 PRELIMINARY; PRT; 468 AA.
ID Q91BA0
AC Q91BA0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE RyPPR2AC protein (Fragment).
GN Name=ryPPR2AC;
OS Potamotrygon motoro (South American freshwater stingray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Hypnosquala; Pristiogalea; Batoida;
OC Myliobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.
OX NCBI_TaxID=86373;

```


Search completed: December 1, 2004, 12:16:20
Job time : 86.8421 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 1, 2004, 12:07:42 ; Search time 19.7573 Seconds
(without alignments)
1134.694 Million cell updates/sec

Title: US-09-095-478a-6_COPY_225_457
Perfect score: 1253
Sequence: 1 QNRDKNRYRDLPLPYDSTRVP.....MIQTKEQYQFCYIVLEVLQ 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	995	79.4	398	2 T08716	protein-tyrosine-p
2	595.5	47.5	2450	2 S71625	protein-tyrosine-p
3	592.5	47.3	2294	2 I67630	protein-tyrosine-p
4	592.5	47.3	2466	2 I67629	protein-tyrosine-p
5	584.5	46.6	2490	1 A54971	protein-tyrosine-p
6	499	39.8	913	1 A41109	protein-tyrosine-p
7	486.5	38.8	2051	2 T30938	receptor tyrosine
8	476.5	38.0	926	1 A41105	protein-tyrosine-p
9	475	37.9	1337	1 I38670	protein-tyrosine-p
10	474.5	37.9	1501	2 I58148	protein-tyrosine-p
11	474.5	37.9	1907	2 S50893	protein-tyrosine-p
12	474.5	37.9	1912	2 A56178	protein-tyrosine-p
13	471	37.6	1499	2 I50212	protein-tyrosine-p
14	469.5	37.5	1997	1 S12050	protein-tyrosine-p
15	468.5	37.4	1863	2 S46217	protein-tyrosine-p
16	468	37.4	1238	2 S68700	protein-tyrosine-p
17	468	37.4	1457	1 A48066	HPTP beta-like tyr
18	467.5	37.3	583	2 S17671	protein-tyrosine-p
19	463	37.0	597	2 B53978	protein-tyrosine-p
20	463	37.0	694	2 A53978	protein-tyrosine-p
21	463	37.0	1187	1 J41155	protein-tyrosine-p
22	461.5	36.8	1262	1 B48758	protein-tyrosine-p
23	461.5	36.8	1496	1 A48758	protein-tyrosine-p
24	461	36.8	382	1 A38191	protein-tyrosine-p
25	461	36.8	1691	1 D54689	protein-tyrosine-p
26	461	36.8	1894	2 C54689	protein-tyrosine-p
27	460.5	36.8	582	2 A57068	protein-tyrosine-p
28	460.5	36.8	1290	2 A56493	leucocyte common a
29	460.5	36.8	1897	1 TDHULK	leucocyte antigen-

30 460.5 36.8 1898 2 S46216
31 460 36.7 387 1 A60345
32 459 36.6 363 1 S14294
33 459 36.6 415 1 A33899
34 458.5 36.6 1176 2 I58345
35 458 36.6 1452 1 S17669
36 457 36.5 1188 1 A57064
37 457 36.5 1216 2 S60613
38 457 36.5 1452 1 S17670
39 456 36.4 405 2 I49372
40 454 36.2 1189 1 JC2366
41 453 36.2 405 2 S68250
42 453 36.2 1187 1 A53661
43 452.5 36.1 1175 2 S51005
44 451.5 36.0 1174 2 I38140
45 450 35.9 356 2 JW0049

ALIGNMENTS

RESULT 1

T08716
protein-tyrosine-phosphatase homolog DKFZp566K0524.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08716
R;Anson, W.; Winkler, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16472
A;Accession: T08716
A;Molecule type: mRNA
A;Residues: 1-398 <ANS>
A;Cross-references: UNIPROT:Q9Y406; EMBL:AL050040
A;Experimental source: fetal kidney; clone DKFZp566K0524
C;Genetics:
A;Note: DKFZp566K0524.1
F;161-379/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 79.4%; Score 995; DB 2; Length 398;
Best Local Similarity 78.0%; Pred. No. 4.3e-85;
Matches 181; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

QY 2 NDKNRYRDLPLPYDSTRVPLGNKKOYNASYIRIVNHEEYFYATQGPLPETIEDFWQM 61
DB 161 NREKNRYRDLPLPYDSTRVPLGSKDYINASYIRIVNCGEYFYATQGPLSTIDDFWQM 220
QY 62 VLENNCNVTAMITRETECGVICKYSWPLSLKEPLEFEHFSVLETFHVTQYFVRFQI 121
DB 221 VLENNSNVTAMITREMEGGIICKYHWPISLKKPLELKHFRVFLFNQYQLQYFIIRMFQV 280
QY 122 VKKSTGKSCVQKHLQFTKWPDHGTTPASADFFIKYRYVRKSHITGTLVHCAGVGRGV 181
DB 281 VEKSTGTSVSHVQLQFTKWPDHGTTPASADSFYIKYRYARKSHLTGPMVHCAGIGRTGV 340
QY 182 FICVDVWFSIAEKNSYDFIMNIVTQKRCORCMIOTKGQYQFCYIVLEVLQ 233
DB 341 FLCVDVWFCVIAVKDCSFNIMDIVAQMRQSRGMVQTKGQYHFCYDIVLEVL 392

RESULT 2

S71625
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 13 - mouse
N;Alternate names: epidermal growth factor-binding protein; serine proteinase
C;Species: Mus musculus (house mouse)
C;Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
C;Accession: S71625; S67987; I81210; I81209; S40290
R;Chida, D.; Kume, T.; Mukoyama, Y.; Tabata, S.; Nomura, N.; Thomas, M.L.; Watanabe, T.
FEBS Lett. 358, 233-239, 1995
A;Title: Characterization of a protein tyrosine phosphatase (RIP) expressed at a very ea
A;Reference number: S71625; MUID:95145716; PMID:7843407
A;Accession: S71625
A;Molecule type: mRNA

C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004

C/Accession: I67630
 C/MaeKawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
 FBS Lett. 337, 200-206, 1994
 A/Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane
 A/Reference number: 153483; MUID:94116679; PMID:8287977
 A/Accession: I67629
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-2466 <RES>
 A/Cross-references: UNIPROT:Q12923; GB:D21210; NID:G452193; PIDN:BAA04751.1; PID:G452194
 C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
 C/Keywords: phosphoric monoester hydrolase
 F:574-868/Domain: protein 4.1 membrane-binding domain homology <B41>
 F:1182-1258/Domain: GLGF domain homology <GLG2>
 F:2046-2265/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 47.5%; Score 595.5; DB 2; Length 2450;
 Best Local Similarity 49.6%; Pred. No. 7.2e-47; Indels 7; Gaps 3;
 Matches 117; Conservative 38; Mismatches 74

QY 1 QNRDKRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
 Db 2202 ENRRKNRYKNILPYDTRVPLGDEGGYINAFIRIPVGTQFEVFIACQGPLTTVGDFWQ 2261

QY 61 MVLNNCNVIAITREIECGVKCYWYPSISL-KEPFEHFSVPLEFHTVQYFTRVVF 119
 Db 2262 MVWEQNSTVIAMMTQVEGEKIKQRYWPSISLGTMTMANERLALLERMQQLKGFIVRVM 2321

QY 120 QIVKSTGSKQCVKHLQTKPDPHGTCTPASAD---FFIKYVYVRKSHITGPLLHVSAGV 176
 Db 2322 ALEIQTEGVHRHSHLNTAFPHDHTPSQPDLLTFISYMRHRS---GPIVTHCSAGI 2378

QY 177 GRIGVFCIVDVVFSIAEKNSYFDIMNIVTQMRKQRCGMITQKEQYFCYVEIVLEVL 232
 Db 2379 GRSGLTICIDVVLGLISQDLBEDISLVRKMRQSHGMVQTEGQYVFCYVILYVL 2434

RESULT 3
 I67630
 protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 3 -
 C/Species: Homo sapiens (man)

C/Accession: I67630
 C/MaeKawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
 FBS Lett. 337, 200-206, 1994
 A/Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane
 A/Reference number: 153483; MUID:94116679; PMID:8287977
 A/Accession: I67630
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-2466 <RES>
 A/Cross-references: UNIPROT:Q12923; GB:D21210; NID:G452193; PIDN:BAA04752.1; PID:G452194
 C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
 C/Keywords: phosphoric monoester hydrolase
 F:574-868/Domain: protein 4.1 membrane-binding domain homology <B41>
 F:1182-1258/Domain: GLGF domain homology <GLG2>
 F:2046-2265/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 47.3%; Score 592.5; DB 2; Length 2294;
 Best Local Similarity 47.6%; Pred. No. 1.3e-46; Indels 1; Gaps 1;
 Matches 111; Conservative 41; Mismatches 80

QY 1 QNRDKRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
 Db 2045 ENRRKNRYKNILPYDAIRVPLGDEGGYINAFIKIPVKEEFYIACQGPLTTVGDFWQ 2104

QY 61 MVLNNCNVIAITREIECGVKCYWYPSISL-KEPFEHFSVPLEFHTVQYFTRVVF 119
 Db 2105 MIWEQKSTVIAMMTQVEGEKIKQRYWPNILKTTMWSNRLALVRMQQLKGFVVRAM 2164

QY 120 QIVKSTGSKQCVKHLQTKPDPHGTCTPASADFFIKYVYVRKSHITGPLLHVSAGVGR 179
 Db 2165 TLEDIQTREVRHSHLNTAFPHDHTPSQPDLLTFISYMRHRSPIITHCSAGIGRS 2224

QY 180 GVFCIVDVVFSIAEKNSYFDIMNIVTQMRKQRCGMITQKEQYFCYVEIVLEVL 232
 Db 2225 GTLICIDVVLGLISQDLBEDISLVRKMRQSHGMVQTEQYIFCYVILYVL 2277

RESULT 4
 I67629
 protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 2 -
 C/Species: Homo sapiens (man)
 C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
 C/Accession: I67629
 R/MaeKawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
 FBS Lett. 337, 200-206, 1994
 A/Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membran
 A/Reference number: 153483; MUID:94116679; PMID:8287977
 A/Accession: I67629
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-2466 <RES>
 A/Cross-references: UNIPROT:Q12923; GB:D21210; NID:G452191; PIDN:BAA04751.1; PID:G45219
 C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
 C/Keywords: phosphoric monoester hydrolase
 F:574-868/Domain: protein 4.1 membrane-binding domain homology <B41>
 F:1354-1430/Domain: GLGF domain homology <GLG2>
 F:2218-2437/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match 47.3%; Score 592.5; DB 2; Length 2466;
 Best Local Similarity 47.6%; Pred. No. 1.4e-46; Indels 1; Gaps 1;
 Matches 111; Conservative 41; Mismatches 80

QY 1 QNRDKRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
 Db 2217 ENRRKNRYKNILPYDAIRVPLGDEGGYINAFIKIPVKEEFYIACQGPLTTVGDFWQ 2276

QY 61 MVLNNCNVIAITREIECGVKCYWYPSISL-KEPFEHFSVPLEFHTVQYFTRVVF 119
 Db 2277 MIWEQKSTVIAMMTQVEGEKIKQRYWPNILKTTMWSNRLALVRMQQLKGFVVRAM 2336

QY 120 QIVKSTGSKQCVKHLQTKPDPHGTCTPASADFFIKYVYVRKSHITGPLLHVSAGVGR 179
 C/Species: Homo sapiens (man)

Db 2337 TLEDIOTREVRHSHLNFAMPDHPDTPSQDDLLLTISYMRHHRSGPIIHTCSAGIGRS 2396

QY 180 GVFICVDVVFSAIEKNSYFDIMNVTQMRKQRCGMITQKEQYQFCVEIIVLEVL 232

Db 2397 GTLICIDVVLGLISQDLDFISDLVRCMLQRHGMVQTDQYIFCYQVILYVL 2449

RESULT 5

A54971

A;Title: protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 1 [M]
N;Alternate names: Fas-associated phosphatase FAP-1; protein-tyrosine-phosphatase hPTP13
C;Species: Homo sapiens (man)
C;Date: 11-Nov-1994 #sequence revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: A54971; A55114; I59595; I53483; S46955
R;Banville, D.; Ahmad, S.; Stocco, R.; Shen, S.H.
J. Biol. Chem. 269, 22320-22327, 1994
A;Title: A novel protein-tyrosine phosphatase with homology to both the cytoskeletal pro
A;Reference number: A54971; MUID:94350988; PMID:8071359
A;Accession: A54971
A;Molecule type: mRNA
A;Residues: 1-2490 <BAN>
A;Cross-references: UNIPROT:Q12923; GB:U12128
A;Note: sequence shown follows authors' translation at positions 62-63
R;Saras, J.; Claesson-Welsh, L.; Heldin, C.H.; Gonez, L.J.
J. Biol. Chem. 269, 24082-24089, 1994
A;Title: Cloning and characterization of PTP11, a protein tyrosine phosphatase with simi
A;Reference number: A55114; MUID:95014139; PMID:7929060
A;Accession: A55114
A;Molecule type: mRNA
A;Residues: 1-61, 'GS', 64-839, 'D', 841-1055, 1075-1133, 'FH', 1136-1210, 'I', 1212-1383, 1389-15
A;Cross-references: GB:X80289; NID:G515030; PIDN:CAA56563.1; PID:G515031
R;Sato, T.; Irie, S.; Kitada, S.; Reed, J.C.
Science 268, 411-415, 1995
A;Title: FAP-1: a protein tyrosine phosphatase that associates with Fas.
A;Reference number: I59595; MUID:95232528; PMID:7536343
A;Accession: I59595
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1279-1888 <RES>
A;Cross-references: GB:I34583; NID:G806291; PIDN:AAC41755.1; PID:G806292
R;Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
FEBS Lett. 337, 200-206, 1994
A;Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane
A;Reference number: I53483; MUID:94116679; PMID:8287977
A;Accession: I53483
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-61, 'GS', 64-839, 'D', 841-1210, 'I', 1212-1383, 1389-2299, 'QM', 2302-2490 <RE2>
A;Cross-references: GB:D21209; NID:G452189; PIDN:BAA04750.1; PID:G452190
C;Genetics:
A;Gene: GDB:PTPN13
A;Cross-references: GDB:306348; OMIM:600267
A;Map position: 4q21.3-4q21.3
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
F;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosi
F;574-868/Domain: protein 4.1 membrane-binding domain homology <B41>
F;1099-1175/Domain: GLGF domain homology <GLG1>
F;1373-1454/Domain: GLGF domain homology <GLG2>
F;1511-1590/Domain: GLGF domain homology <GLG3>
F;1799-1870/Domain: GLGF domain homology <GLG4>
F;1893-1967/Domain: GLGF domain homology <GLG5>
F;2242-2461/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;2413/Active site: Cys (phosphocysteine intermediate) #status predicted
F;2419/Binding site: substrate phosphate (Arg) #status predicted

Query Match 46.6%; Score 584.5; DB 1; Length 2490;
Best Local Similarity 46.8%; Pred. No. 7.8e-46;
Matches 109; Conservative 43; Mismatches 80; Indels 1; Gaps 1;

QY 1 QNRDKNRYRDIPLVDSTRVPLGKNKDYINASYIRVNHHEEYFYIATQGPLPTEI 60

Db 2241 ENRRKNRYKILPYDATRVPLDGEVGYINASFIKIPVGKEEFYIACQGLPTITVGDFWR 2300

QY 61 MVLNNCNVMIATRIEIEGVIKCYSWPISL-KEPLEEHEFSVFLETFHTVQYETVRVF 119

Db 2301 VIMEQKSTVIAMWTOEVEGEKIKORYWPNILGKTTMVNSNRLLALVRWQQLGFGVVRAM 2360

QY 120 QIVKSKSTGKSQCWKHLQFTKWDHGTTPASADFFIKYRVYVRKSHITGPIILVHCSAGVGR 179

Db 2361 TLEDIOTREVRHSHLNFAMPDHPDTPSQDDLLLTISYMRHHRSGPIIHTCSAGIGRS 2420

QY 180 GVFICVDVVFSAIEKNSYFDIMNVTQMRKQRCGMITQKEQYQFCVEIIVLEVL 232

Db 2421 GTLICIDVVLGLISQDLDFISDLVRCMLQRHGMVQTDQYIFCYQVILYVL 2473

RESULT 6

A41109

A;Title: protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN3, nonreceptor type 3 [validated] - human
N;Alternate names: PTPH1
C;Species: Homo sapiens (man)
C;Date: 27-Mar-1992 #sequence_revision 02-May-1994 #text_change 09-Jul-2004
C;Accession: A41109; I55698
R;Yang, Q.; Tonks, N.K.
Proc. Natl. Acad. Sci. U.S.A. 88, 5949-5953, 1991
A;Title: Isolation of a cDNA clone encoding a human protein-tyrosine phosphatase with ho
A;Reference number: A41109; MUID:91296738; PMID:1648725
A;Accession: A41109
A;Molecule type: mRNA
A;Residues: 1-913 <YAN>
A;Cross-references: UNIPROT:P26045; GB:M64572; NID:G179912; PIDN:AAA35647.1; PID:G179913
R;Ikuta, S.; Itoh, F.; Hinoda, Y.; Toyota, M.; Makiguchi, Y.; Imai, K.; Yachi, A.
J. Gastroenterol. 29, 727-732, 1994
A;Title: Expression of cytoskeletal-associated protein tyrosine phosphatase PTPH1 mRNA i
A;Reference number: I55698; MUID:95179278; PMID:7874267
A;Accession: I55698
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 899-913 <RES>
A;Cross-references: GB:S76309; NID:G9131165; PIDN:AAB33583.1; PID:G9131166
C;Genetics:
A;Gene: GDB:PTPN3
A;Cross-references: GDB:131386; OMIM:176877
A;Map position: 9q31-9q31
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology; p
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
F;31-308/Domain: protein 4.1 membrane-binding domain homology <B41>
F;516-590/Domain: GLGF domain homology <GLG>
F;670-890/Domain: protein-tyrosine-phosphatase homology <PTP>
F;842/Active site: Cys (phosphocysteine intermediate) #status predicted
F;848/Binding site: substrate phosphate (Arg) #status predicted

Query Match 39.8%; Score 499; DB 1; Length 913;
Best Local Similarity 42.0%; Pred. No. 2.2e-38;
Matches 102; Conservative 38; Mismatches 85; Indels 18; Gaps 5;

QY 1 QNRDKNRYRDIPLVDSTRVPLGKNKDYINASYIRVNHHEEYFYIATQGPLPE 53

Db 669 QNLDKNRYKDVLPDYTRVLLQGNEDYINASYINMEIPAANLVNK-----YIATQGPLPH 723

QY 54 TIEDFWQVLENNCNVMIATRIEIEGVIKCYSWPISLKEPLEFEH--FSVLETFHTVT 111

Db 724 TCAQFWQVVDQKLSLIVMTLTTERGRTKCHQYWP---DPPDVNHHGGFHIQCQSEDC 780

QY 112 QYFTVRVQIVKSKSTGKSQCWKHLQFTKWDHGTTPASADFFIKYRVYVRKSHIT-TGPIILV 170

Db 781 IAVYSREMLVTNTQTGEEHTVTHLQYVAMPDHGIPDDSSDFLEFFVNVYVSLRVDSEFVLV 840

QY 171 HCSAGVGRGTGVFTCDVDFVSAIEKNSYFDIMNVTQMRKQRCGMITQKEQYQFCYIVLE 230

Db 841 HCSAGIGRTGVLTMTMETACLTENRNLPIYPLDIVRKNRQDRAMWVQTSQYKVFCEAILR 900

QY 231 VLQ 233

Db 901 VYE 903

RESULT 7

T30938
C:Species: Hirudo medicinalis (medicinal leech)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30938
R:Gershon, T.R.; Baker, M.; Nitabach, M.; Wu, P.; Macagno, E.R.
submitted to the EMBL Data Library, December 1997
A:Description: Two receptor tyrosine phosphatases of the LAR subfamily are expressed in A:Reference number: 220939
A:Accession: T30938
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2051 <GER>
A:Cross-references: UNIPROT:O44328; EMBL:AF017083; NID:G2695654; PID:G2695655; PIDN:AA95
C:Genetics:
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; ogy

Query Match 38.8%; Score 486.5; DB 2; Length 2051;
Best Local Similarity 41.1%; Pred. No. 8.7e-37;
Matches 99; Conservative 45; Mismatches 82; Indels 15; Gaps 6;

QY 2 NRDKNRYRDLPYDSTRVPLG-----KNKDYINASYIRIVNHEEYFYIATQGLPETIE 56

Db 1808 NKQKRLNVLNPLVETTRKVLQPIRGVDSYIINASFID--GYRVRAYIATQGLPDTVE 1865

QY 57 DFQWVLNCCNVIAMITREIEGVKICYSYWPISLKEPLEFHFHSVF-LETFHVTQYFT 115

Db 1866 DFRALWESNCNIIIVMLTKLEMGRENCHQWYP--SERSARYQVFFVDDPLAEYNMPOYI- 1922

QY 116 VRVPIQIVKSTGKSCQVHLOFTKWPDHGTPASADFFIKVYRVYRKSH-----ITGPLLHV 171

Db 1923 LRFKVTARDGQSRTRQPLTDWPEQGVSTGDFGIDFGITGQTHKTEQFGQEGPTAVH 1982

QY 172 CSAGVGTGVTFCVDDVVFSAIEKNYSFDIMNIVTQMKQKRCGMQTKQYQFCYVEIVLE 231

Db 1983 CSAGVGTGVTFTLSILVLRMRFEAGVDVFTQVNVLTQPGMVQTEQYAFCAALEY 2042

QY 232 L 232

Db 2043 L 2043

RESULT 8

A41105
protein-tyrosine-phosphatase (EC 3.1.1.3.48) PTPN4, nonreceptor type 4 [validated] - human
N:Alternate names: pTPase MEG
C:Species: Homo sapiens (man)
C:Date: 20-Mar-1992 #sequence_revision 02-May-1994 #text_change 09-Jul-2004
C:Accession: A41105
R:Gu, M.; York, J.D.; Warshawsky, I.; Majerus, P.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 5867-5871, 1991
A:Title: Identification, cloning, and expression of a cytosolic megakaryocyte protein-ty A:Reference number: A41105; MUID:91288564; PMID:1648233
A:Accession: A41105
A:Molecule type: mRNA
A:Residues: 1-926 <GUA>
A:Cross-references: UNIPROT:P29074; GB:M68941; NID:G190747; PIDN:AAA36530.1; PID:G190748
A:Experimental source: megakaryocytes, cell line MEG-10
C:Genetics:
A:Gene: GDB:PTPN4
A:Cross-references: GDB:131387; OMIM:176878
A:Map position: 9q31-9q31
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology; P C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas E:31-308/Domain: protein 4.1 membrane-binding domain homology <B41>
F:523-597/Domain: GLGF domain homology <GLG>
F:679-900/Domain: protein-tyrosine-phosphatase homology <PTP>
F:852/Active site: Cys (phosphocysteine intermediate) #status predicted
F:858/Binding site: substrate phosphate (Arg) #status predicted

F;1245/Binding site: substrate phosphate (Arg) #status predicted

Query Match 37.9%; Score 475; DB 1; Length 1337;
 Best Local Similarity 40.7%; Pred. No. 6.1e-36;
 Matches 98; Conservative 48; Mismatches 83; Indels 12; Gaps 5;

QY 1 QNRDKNRYDILPYDSTRVPLG-----KNKDYINASYIRIVNHEEYFYIATQGPLPETIE 56
 DB 1064 ENRGKNRYNVLPSYDISTRVPLG-----KNKDYINASYIRIVNHEEYFYIATQGPLPETIE 1121

QY 57 DFQWLVNLCNVMIATREIECGVTKCYSWPISLKEPLEFHFHSVFLETHVTQYFTV 116
 DB 1122 DFQWLVNLCNVMIATREIECGVTKCYSWPISLKEPLEFHFHSVFLETHVTQYFTV 1179

QY 117 RVFQIVKSTGKSCQVKKHLOFTKWPDPHTGTPASADFFIKYVYVRKSH---ITGPLLHV 172
 DB 1180 RDTVKNIQTSESHPLRQFHFTSWPDGHPDVTDLINFRYLVRDYMKSPPSPILVHC 1239

QY 173 SAGVGRGTGVCVDVWFSIAEKNYSDIMNIVTQMRKQRCGMIOQKEQYFCYEVILEV 232
 DB 1240 SAGVGRGTGFIADRLIYQIENENTVDVVGIVYDLRMHRPLMVQTEDQYVFLNQCVLDIV 1299

QY 233 Q 233
 DB 1300 R 1300

RESULT 10
 I58148
 protein-tyrosine-phosphatase (EC 3.1.3.48) 2B, splice form LAR - rat
 N;Alternate names: leukocyte common antigen-related phosphatase
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C;Accession: I58148; S46218
 R;Walton, K.M.; Martell, K.J.; Kwak, S.P.; Dixon, J.E.; Largent, B.L.
 Neuron 11, 387-400, 1993
 A;Title: A novel receptor-type protein tyrosine phosphatase is expressed during neurogen
 A;Reference number: I58148; MUID:93357030; PMID:8352946
 A;Accession: I58148
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-1501 <WAL>
 A;Cross-references: UNIPROT:Q64605; GB:L19933; NID:g310242; PIDN:AAA42309.1; PID:g310243
 A;Note: in Genbank entry RATTYPHOS, release 113.0, the source is designated as Rattus n
 R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
 Biochem. J. 302, 39-47, 1994
 A;Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-pho
 A;Reference number: S46216; MUID:94347119; PMID:8068021
 A;Accession: S46218
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-1501 <ZHA>
 A;Cross-references: EMBL:L12329; NID:g294573; PIDN:AAAC37657.1; PID:g294574
 C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
 ogy
 C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosi
 F;47-109/Domain: immunoglobulin homology <IMM1>
 F;149-209/Domain: immunoglobulin homology <IMM2>
 F;246-300/Domain: immunoglobulin homology <IMM3>
 F;413-506/Domain: fibronectin type III repeat homology <3PR>
 F;882-1501/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F;969-1190/Domain: protein-tyrosine-phosphatase homology <PTP1>
 F;1258-1481/Domain: protein-tyrosine-phosphatase homology <PTP2>
 F;1142/Active site: Cys (phosphocysteine intermediate) #link PTP1 #status predicted
 F;1148/Binding site: substrate phosphate (Arg) #link PTP1 #status predicted
 F;1433/Active site: Cys (phosphocysteine intermediate) #link PTP2 #status predicted
 F;1439/Binding site: substrate phosphate (Arg) #link PTP2 #status predicted

Query Match 37.9%; Score 474.5; DB 2; Length 1501;
 Best Local Similarity 41.1%; Pred. No. 7.9e-36;
 Matches 99; Conservative 46; Mismatches 81; Indels 15; Gaps 6;

QY 2 NRDKNRYDILPYDSTRVPLG-----KNKDYINASYIRIVNHEEYFYIATQGPLPETIE 56

DB 1258 NFKKRLNVLPESSRVCLQPIRGVSGSDYNASFDID--GYRQOKAYIATQGPLAETTE 1315
 QY 57 DFQWLVNLCNVMIATREIECGVTKCYSWPISLKEPLEFHFHSVF-LETFHVTQYFT 115
 DB 1316 DFQWLVNLCNVMIATREIECGVTKCYSWPISLKEPLEFHFHSVF--AERSARYQYFVVDPMAYNMPQYI- 1372

QY 116 VRVFOIVKSTGKSCQVKKHLOFTKWPDPHTGTPASADFFIKYVYVRKSH---ITGPLLHV 171
 DB 1373 LREFKVTARDGQSRVRFQFTDMPQAPKSGGFIQGVHKTKEQFGDGFISVH 1432

QY 172 CSAGVGRGTGVCVDVWFSIAEKNYSDIMNIVTQMRKQRCGMIOQKEQYFCYEVILEV 231
 DB 1433 CSAGVGRGTGVCFTLSVLRMRYEGVWDIFQIVKVLRTQRPAMVQTEDEVYFCFQAALV 1492

QY 232 L 232
 DB 1493 L 1493

RESULT 11
 S50893
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type sigma precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
 C;Accession: S50893; S40281
 R;Wagner, J.; Boerboom, D.; Tremblay, M.L.
 Eur. J. Biochem. 226, 773-782, 1994
 A;Title: Molecular cloning and tissue-specific RNA processing of a murine receptor-type
 A;Reference number: S50893; MUID:95112841; PMID:7529177
 A;Accession: S50893
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1907 <WAG>
 A;Cross-references: UNIPROT:Q64494; EMBL:X82288; NID:g587483; PIDN:CAA57732.1; PID:g5874
 R;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
 Submitted to the EMBL Data Library, June 1993
 A;Description: Assessment of the expression levels of murine protein-tyrosine phosphatas
 A;Reference number: S40280
 A;Accession: S40281
 A;Molecule type: mRNA
 A;Residues: 1441-1501, 'E', 1503-1546 <HEN>
 A;Cross-references: EMBL:Z23050; NID:g438137; PIDN:CRA80585.1; PID:g438138
 C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
 ogy
 C;Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
 F;149-209/Domain: immunoglobulin homology <IMM1>
 F;246-300/Domain: immunoglobulin homology <IMM2>
 F;413-506/Domain: fibronectin type III repeat homology <3PR>
 F;1288-1907/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F;1375-1596/Domain: protein-tyrosine-phosphatase homology <PTP1>
 F;1664-1887/Domain: protein-tyrosine-phosphatase homology <PTP2>
 F;1548/Active site: Cys (phosphocysteine intermediate) #status predicted
 F;1554/Binding site: substrate phosphate (Arg) #status predicted
 F;1839/Active site: Cys (phosphocysteine intermediate) #status predicted
 F;1845/Binding site: substrate phosphate (Arg) #status predicted

Query Match 37.9%; Score 474.5; DB 2; Length 1907;
 Best Local Similarity 41.1%; Pred. No. 1e-35;
 Matches 99; Conservative 46; Mismatches 81; Indels 15; Gaps 6;

QY 2 NRDKNRYDILPYDSTRVPLG-----KNKDYINASYIRIVNHEEYFYIATQGPLPETIE 56
 DB 1664 NFKKRLNVLPESSRVCLQPIRGVSGSDYNASFDID--GYRQOKAYIATQGPLAETTE 1721

QY 57 DFQWLVNLCNVMIATREIECGVTKCYSWPISLKEPLEFHFHSVF-LETFHVTQYFT 115
 DB 1722 DFQWLVNLCNVMIATREIECGVTKCYSWPISLKEPLEFHFHSVF--AERSARYQYFVVDPMAYNMPQYI- 1778

QY 116 VRVFOIVKSTGKSCQVKKHLOFTKWPDPHTGTPASADFFIKYVYVRKSH---ITGPLLHV 171
 DB 1779 LREFKVTARDGQSRVRFQFTDMPQAPKSGGFIQGVHKTKEQFGDGFISVH 1838

S12050
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type beta precursor - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S12050; S15818; S15819
R:Krueger, N.X.; Streuli, M.; Saito, H.
EMBO J. 9, 3241-3252, 1990
A:Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatase
A:Reference number: S12049; MUID:91006018; PMID:2170109
A:Accession: S12050
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-1997 <KRU>
A:Cross-references: UNIPROT:P23467; GB:X54131; NID:g35787; PIDN:CAA38066.1; PID:g35788
R:de Vries, L.; Li, R.Y.; Ragab, A.; Ragab-Thomas, J.M.F.; Chap, H.
FEBS Lett. 282, 285-288, 1991
A:Title: Expression of a truncated protein-tyrosine phosphatase mRNA in human lung.
A:Reference number: S15818; MUID:91243813; PMID:1645282
A:Accession: S15818
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1872-1911, 'VHMVLQK' <VRI>
A:Accession: S15819
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1872-1997 <VR2>
C:Genetics:
A:Gene: GDB:PTPRB; PTPB
A:Cross-references: GDB:127352; OMIM:176882
A:Map position: 12q15-12q21
C:Superfamily: protein-tyrosine-phosphatase, receptor type beta; fibronectin type III repeat
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-1997/Product: protein-tyrosine-phosphatase, receptor type beta #status predicted <M>
F:23-1625/Domain: extracellular #status predicted <EXT>
F:1626-1642/Domain: transmembrane #status predicted <TM>
F:1643-1997/Domain: intracellular #status predicted <INT>
F:1727-1952/Domain: protein-tyrosine-phosphatase homology <PTP>
F:1904/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1910/Binding site: substrate phosphate (Arg) #status predicted
Query Match 37.5%; Score 469.5; DB 1; Length 1997;
Best Local Similarity 41.2%; Pred. No. 3.2e-35;
Matches 100; Conservative 43; Mismatches 87; Indels 13; Gaps 5;
QY 1 QNRDKNRYRDLIPYDSTRVPLGK-----NKDYINASIRIVNHEEYFYIATQGLPETI 55
Db 1726 ENRGKRNINILPYDATRVKLSNVDDDDPCSDYINASYIPGNFRFE--YIVTQGLPGTK 1783
QY 56 EDEWQVLENNCNVIAITREIEGVIKCYWPISEKLEPFEHFSVFLETHVTQYFT 115
Db 1784 DDFWKWQWQNVNINIVMTQCVKEGRVKCDHYWPAQ--QDSLYYGDLLQLMSVLPPEWT 1842
QY 116 VRVQIV-KKSTGKSCQVKKLQFTKPDHGTTPASADFFIKYVR-----YVRKSHITGPLL 170
Db 1843 IREFKICGEBQDAHLIRHFHYTWVDHGVPTTQSLIQFVIRVDRYINRSPAGPTVV 1902
QY 171 HCSAGVGRTVGTCVVDVVFSAIEKNYSFDMNIVTQMRKQRCGMIOKEQYQFCYEVLE 230
Db 1903 HCSAGVGRTVGTCVVDVVFSAIEKNYSFDMNIVTQMRKQRCGMIOKEQYQFCYEVLE 230
QY 231 VLQ 233
Db 1963 VLR 1965
RESULT 15
S46217
protein-tyrosine-phosphatase (EC 3.1.3.48) type sigma precursor - rat
N:Alternate names: leukocyte common antigen-related phosphatase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S46217; S51174; A49104

R:Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
Biochem. J. 302, 39-47, 1994
A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phosphatase
A:Reference number: S46216; MUID:94347119; PMID:8068021
A:Accession: S46217
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1863 <ZHA>
A:Cross-references: UNIPROT:Q64605; EMBL:L11587
R:Goldstein, B.J.
submitted to the EMBL Data Library, February 1993
A:Reference number: S51174
A:Accession: S51174
A:Molecule type: mRNA
A:Residues: 1-1788, 'G', 1790-1863 <GOL>
A:Cross-references: EMBL:L11587; NID:g205134; PIDN:AAC37656.1; PID:g205135
R:Yan, H.; Grossman, A.; Wang, H.; D'Eustachio, P.; Mossie, K.; Musacchio, J.M.; Silven
J. Biol. Chem. 268, 24880-24886, 1993
A:Title: A novel receptor tyrosine phosphatase-sigma that is highly expressed in the ne
A:Reference number: A49104; MUID:94043351; PMID:8227050
A:Accession: A49104
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-596, 'R', 598-603, 'I', 967-1788, 'G', 1790-1863 <YAN>
A:Experimental source: Brain
A:Note: sequence extracted from NCBI backbone (NCBIP:139669)
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
QY 2 NRDKNRYRDLIPYDSTRVPLG-----NKDYINASIRIVNHEEYFYIATQGLPETIE 56
Db 1620 NKFNRLVNLIPYESSRVLQPIRGVEGSDYINASFID--GYRQKAYIATQGLPETIE 1677
QY 57 DFWQVLENNCNVIAITREIEGVIKCYWPISEKLEPFEHFSVF-LETHVTQYFT 115
Db 1678 DFWALWENNSTIVMLTKLRNGRCKHQYWP--NERSARYQYFVDPMAEYIMQYI- 1734
QY 116 VRVQIV-KKSTGKSCQVKKLQFTKPDHGTTPASADFFIKYVRKSH-----ITGPLL 171
Db 1735 LREFKVTVDARDGSRVTRQFQFTDWEQAPKSGEGFIDFIGVHVKTEQFGQDAPISVH 1794
QY 172 CSAGVGRTVGTCVVDVVFSAIEKNYSFDMNIVTQMRKQRCGMIOKEQYQFCYEVLE 231
Db 1795 CSAGVGRTVGTCVVDVVFSAIEKNYSFDMNIVTQMRKQRCGMIOKEQYQFCYEVLE 231
QY 232 L 232
Db 1855 L 1855
Search completed: December 1, 2004, 12:17:28
Job time : 20.7573 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 1, 2004, 12:16:33 ; Search time 424.441 Seconds
(without alignments)
195.771 Million cell updates/sec

Title: US-09-095-478A-6_COPY_225_457

Perfect score: 1253

Sequence: 1 QNRDKNRYRDLIPYDSTRVP.....MIQTKEQYQFCYIVLEVLQ 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/prodata/2/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/2/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/2/pubpaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/2/pubpaa/US10_PUBCOMB.pep.*
- 17: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1253	100.0	354	10	US-09-095-478-6
2	1253	100.0	379	10	US-09-095-478-8
3	1253	100.0	426	10	US-09-095-478-1
4	1253	100.0	463	10	US-09-095-478-2
5	1174	93.7	412	10	US-09-095-478-3
6	1003	80.0	420	15	US-10-311-764-4
7	668	53.3	122	10	US-09-095-478-4
8	598.5	47.8	381	10	US-09-095-478-7
9	592.5	47.3	358	10	US-09-095-478-9
10	592.5	47.3	1267	14	US-10-060-065-35
11	592.5	47.3	1267	14	US-10-059-585-56
12	592.5	47.3	2466	14	US-10-177-980-12
13	592.5	47.3	2466	17	US-10-795-148-2

14	592.5	47.3	2485	9	US-09-802-669-46
15	592.5	47.3	2485	15	US-10-619-220-46
16	592.5	47.3	2485	16	US-10-408-765A-1349
17	566	45.2	122	10	US-09-095-478-5
18	564	45.0	263	15	US-10-087-684-93
19	564	45.0	263	15	US-10-087-684-93
20	538	42.9	235	15	US-10-087-684-94
21	538	42.9	235	15	US-10-218-779-94
22	538	42.9	235	15	US-10-072-012-819
23	499	39.8	913	9	US-09-848-294-2
24	499	39.8	913	14	US-10-293-231-2
25	499	39.8	913	14	US-10-366-547-38
26	494	39.4	244	9	US-09-848-294-7
27	494	39.4	244	14	US-10-293-231-7
28	488.5	39.0	1948	9	US-09-808-602-55
29	488.5	39.0	1948	10	US-09-800-198-45
30	488	38.9	703	14	US-10-366-547-40
31	487	38.9	291	9	US-09-788-626-22
32	483.5	38.6	1502	9	US-09-808-602-54
33	483.5	38.6	1502	10	US-09-800-198-44
34	482.5	38.5	264	14	US-10-245-539-6
35	475	37.9	341	16	US-10-723-606-3
36	475	37.9	1337	14	US-10-390-501-2
37	475	37.9	1337	14	US-10-366-547-42
38	475	37.9	1337	14	US-10-366-547-44
39	475	37.9	1337	16	US-10-723-606-2
40	474.5	37.9	344	16	US-10-408-765A-1670
41	469.5	37.5	312	15	US-10-634-027-6
42	469.5	37.5	319	15	US-10-634-027-7
43	469.5	37.5	336	15	US-10-634-027-4
44	469.5	37.5	1997	10	US-09-909-567B-54
45	469.5	37.5	1997	15	US-10-634-027-2

ALIGNMENTS

RESULT 1

US-09-095-478-6
; Sequence 6, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUPT05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-09-095-478-6

Query Match 100.0%; Score 1253; DB 10; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.4e-125;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
DB 118 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 177
QY 61 MVLNNCNVIAITRIIECGVIKCYSWPISLKEPLEFEHFSVLETFHVTQYFTVRVFG 120
DB 178 MVLNNCNVIAITRIIECGVIKCYSWPISLKEPLEFEHFSVLETFHVTQYFTVRVFG 237
QY 121 IVKSTGKSCQVHLOFTKWPDHGTSPASADFFIKYVRYVRKSHITGPLLHVCSSAGVGRG 180
DB 238 IVKSTGKSCQVHLOFTKWPDHGTSPASADFFIKYVRYVRKSHITGPLLHVCSSAGVGRG 297
QY 181 VFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 233
DB 298 VFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 350

RESULT 2
US-09-095-478-8
Sequence 8, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPT05 AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Fast-SEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-09-095-478-8

Query Match 100.0%; Score 1253; DB 10; Length 379;
Best Local Similarity 100.0%; Pred. No. 1.6e-125;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
DB 143 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 202
QY 61 MVLNNCNVIAITRIIECGVIKCYSWPISLKEPLEFEHFSVLETFHVTQYFTVRVFG 120
DB 203 MVLNNCNVIAITRIIECGVIKCYSWPISLKEPLEFEHFSVLETFHVTQYFTVRVFG 262
QY 121 IVKSTGKSCQVHLOFTKWPDHGTSPASADFFIKYVRYVRKSHITGPLLHVCSSAGVGRG 180
DB 263 IVKSTGKSCQVHLOFTKWPDHGTSPASADFFIKYVRYVRKSHITGPLLHVCSSAGVGRG 322
QY 181 VFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 233
DB 323 VFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 375

RESULT 3
US-09-095-478-1
Sequence 1, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPT05 AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Fast-SEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

```
;
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-09-095-478-1

Query Match      100.0%; Score 1253; DB 10; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.8e-125;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNRDKNRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
Db 188 QNRDKNRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 247
Qy 61 MVLNNCNVIMATIREIECGVIKCYSWPISLKEPLEFHFHVSFLETFHVTQYFTVRVFQ 120
Db 248 MVLNNCNVIMATIREIECGVIKCYSWPISLKEPLEFHFHVSFLETFHVTQYFTVRVFQ 307
Qy 121 IVKSTGKSCVKGHLOFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLHVCAGVGRGTG 180
Db 308 IVKSTGKSCVKGHLOFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLHVCAGVGRGTG 367
Qy 181 VFCVDVWFSIAEKNSFDMINIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 233
Db 368 VFCVDVWFSIAEKNSFDMINIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 420

RESULT 4
US-09-095-478-2
; Sequence 2, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 463 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

;
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-09-095-478-2

Query Match      100.0%; Score 1253; DB 10; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.8e-125;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNRDKNRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
Db 188 QNRDKNRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 247
Qy 61 MVLNNCNVIMATIREIECGVIKCYSWPISLKEPLEFHFHVSFLETFHVTQYFTVRVFQ 120
Db 248 MVLNNCNVIMATIREIECGVIKCYSWPISLKEPLEFHFHVSFLETFHVTQYFTVRVFQ 307
Qy 121 IVKSTGKSCVKGHLOFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLHVCAGVGRGTG 180
Db 308 IVKSTGKSCVKGHLOFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLHVCAGVGRGTG 367
Qy 181 VFCVDVWFSIAEKNSFDMINIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 233
Db 368 VFCVDVWFSIAEKNSFDMINIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 420

RESULT 5
US-09-095-478-3
; Sequence 3, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 412 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-09-095-478-3
```

Query Match 93.7%; Score 1174; DB 10; Length 412;
Best Local Similarity 100.0%; Pred. No. 5.2e-117;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QNRDKNRYDILPYDSTRVPLGKNDYINASYIRIVNHEEYFYATQGLPETIEDFWQ 60
188 QNRDKNRYDILPYDSTRVPLGKNDYINASYIRIVNHEEYFYATQGLPETIEDFWQ 247

61 MVLNNCNVAMITREIEGVIKCYWPISLKEPFEHFSVLETFHVTOYFTVRVQ 120
248 MVLNNCNVAMITREIEGVIKCYWPISLKEPFEHFSVLETFHVTOYFTVRVQ 307

121 IVKSTGKSCQVKHLQFTKMPDHGTPTASADFFIKYVRYVRKSHITGPLLHVCSAGVGRIG 180
308 IVKSTGKSCQVKHLQFTKMPDHGTPTASADFFIKYVRYVRKSHITGPLLHVCSAGVGRIG 367

181 VFICVDVWFAIEKNYSFDIMNVTQMRKORCGMIQTK 218
368 VFICVDVWFAIEKNYSFDIMNVTQMRKORCGMIQTK 405

RESULT 6
US-10-311-764-4
; Sequence 4, Application US/10311764
; Publication No. US20040023245A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; AU-YOUNG, Janice K.
; APPLICANT: BAUGHN, Mariah R.; DING, Li
; APPLICANT: ELLIOTT, Vicki S.; GANDHI, Ameena R.
; APPLICANT: GRIFFIN, Jennifer A.; HAFALIA, April J.A.
; APPLICANT: KEARNEY, Liam; LEE, Ernestine A.
; APPLICANT: LU, Yan; NGUYEN, Dannel B.
; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Javalaxmi
; APPLICANT: REDDY, Roopa M.; SANJANWALA, Madhusudan M.
; APPLICANT: STEWART, Elizabeth A.; TANG, Y. Tom
; APPLICANT: THORNTON, Michael B.; TRIBOULEY, Catherine M.
; APPLICANT: CHAWLA, Narinder K.; YANG, Junning
; APPLICANT: YAO, Monique G.; YUE, Henry
; TITLE OF INVENTION: PROTEIN PHOSPHATASES
; FILE REFERENCE: PI-0126 USN
; CURRENT APPLICATION NUMBER: US/10/311,764
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/19442
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/212,447
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/213,746
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 60/215,210
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/216,529
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: US 60/218,080
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/220,117
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023245A1 7476861CD1
US-10-311-764-4

Query Match 80.0%; Score 1003; DB 15; Length 420;
Best Local Similarity 78.9%; Pred. No. 1.2e-98;
Matches 193; Conservative 24; Mismatches 25; Indels 0; Gaps 0;

2 NRDKNRYDILPYDSTRVPLGKNDYINASYIRIVNHEEYFYATQGLPETIEDFWQ 61

183 NREKNRYDILPYDSTRVPLGSKDYINASYIRIVNCGEYFYIATQGLLSTIDDFWQ 242
62 VLENNCNVAMITREIEGVIKCYWPISLKEPFEHFSVLETFHVTOYFTVRVQ 121
243 VLENNCNVAMITREIEGVIKCYWPISLKEPFEHFSVLETFHVTOYFTVRVQ 302

122 VKKSTGKSCQVKHLQFTKMPDHGTPTASADFFIKYVRYVRKSHITGPLLHVCSAGVGRIG 181
303 VKKSTGKSCQVKHLQFTKMPDHGTPTASADFFIKYVRYVRKSHITGPMVHVCSAGIGRTG 362

182 FICVDVWFAIEKNYSFDIMNVTQMRKORCGMIQTKQCYEIVLVLQ 233
363 FLCVDVWFAIVKNCSEINMIDIVAQMRQORSGMWQTKQYHFCYDVLVLE 414

RESULT 7
US-09-095-478-4
; Sequence 4, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUPT05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon and Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-095-478-4

Query Match 53.3%; Score 668; DB 10; Length 122;
Best Local Similarity 100.0%; Pred. No. 2e-63;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

57 DFQWVLENNCNVAMITREIEGVIKCYWPISLKEPFEHFSVLETFHVTOYFTV 116
1 DFQWVLENNCNVAMITREIEGVIKCYWPISLKEPFEHFSVLETFHVTOYFTV 60

Qy 117 RVFQIVKSKGSCQVKHLQFTKWPDHGTTPASADFFIKYVRYVRKSHITGPLLHVCAGV 176
Db 61 RVFQIVKSKGSCQVKHLQFTKWPDHGTTPASADFFIKYVRYVRKSHITGPLLHVCAGV 120
Qy 177 GR 178
Db 121 GR 122

RESULT 8
US-09-095-478-7
; Sequence 7, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-095-478-7

Query Match 47.8%; Score 598.5; DB 10; Length 381;
Best Local Similarity 50.0%; Pred. No. 2.6e-55;
Matches 118; Conservative 37; Mismatches 74; Indels 7; Gaps 3;
Qy 1 QNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIWNHEEYFYIATQGPLPETHEDFWQ 60
Db 144 ENRRKNRYKNILPYDTRVPLGDEGGYINASFIRIPVGTQEFVYIACQGPLTTVGDFWQ 203
Qy 61 MVLNNCNVIAITREIECGVIKCYSWPISL-KEPPEFEHFSVLETHVTVQYTVRVF 119
Db 204 MWEQNSTVIAMTQVEGEKIKCORYWPSILGTTMANERLALLRMQQLKGFIVRM 263
Qy 120 QIVKSKTGKSCQVKHLQFTKWPDHGTTPASAD---FFIKYVRYVRKSHITGPLLHVCAGV 176
Db 264 ALEDIQTEVRHISHLNFTAWPDHDTSPQDDLLTFISYMRHRS---GPVITHCSAGI 320

Qy 177 GRTGVFCVDVVFSAIEKNYSFDMINIVTQMRKQRCMIQTKEQYQFCYEIVLEVL 232
Db 321 GRSGLTICIDWLGLISQDLEFDISLVRMQLQRHGMVQTEGOYVFCYQVILVVL 376

RESULT 9
US-09-095-478-9
; Sequence 9, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-095-478-9

Query Match 47.3%; Score 592.5; DB 10; Length 358;
Best Local Similarity 47.6%; Pred. No. 1e-54;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;
Qy 1 QNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIWNHEEYFYIATQGPLPETHEDFWQ 60
Db 121 ENRRKNRYKNILPYDTRVPLGDEGGYINASFIRIPVGTQEFVYIACQGPLTTVGDFWQ 180
Qy 61 MVLNNCNVIAITREIECGVIKCYSWPISL-KEPPEFEHFSVLETHVTVQYTVRVF 119
Db 181 MIWEQNSTVIAMTQVEGEKIKCORYWPSILGTTMANERLALLRMQQLKGFIVRM 240
Qy 120 QIVKSKTGKSCQVKHLQFTKWPDHGTTPASADFFIKYVRYVRKSHITGPLLHVCAGV 179
Db 241 TLEDIQTEVRHISHLNFTAWPDHDTSPQDDLLTFISYMRHRSGLIITHCSAGIRS 300
Qy 180 GVFCVDVVFSAIEKNYSFDMINIVTQMRKQRCMIQTKEQYQFCYEIVLEVL 232

Db 301 GTLICIDVVLGLISQDLDFDISDLVRCMLRQHRGMVQTEDQYIFCYQVILYVL 353

RESULT 10

US-10-060-065-35

Sequence 35, Application US/10060065

Publication NO. US20030017480A1

GENERAL INFORMATION:

APPLICANT: Toshio Ota

APPLICANT: Takao Isogai

APPLICANT: Tetsuo Nishikawa

APPLICANT: Koji Hayashi

APPLICANT: Kaoru Otsuka

APPLICANT: Jun-Ichi Yamamoto

APPLICANT: Shizuko Ishii

APPLICANT: Tomoyasu Sugiyama

APPLICANT: Ai Wakamatsu

APPLICANT: Keiichi Nagai

APPLICANT: Tetsuji Otsuki

APPLICANT: Shin-Ichi Funahashi

APPLICANT: Chiaki Senoo

APPLICANT: Jun-Ichi Nezu

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE

FILE REFERENCE: 06501-095002

CURRENT APPLICATION NUMBER: US/10/060,065

CURRENT FILING DATE: 2002-01-29

PRIOR APPLICATION NUMBER: PCT/JP00/05061

PRIOR FILING DATE: 2000-07-28

PRIOR APPLICATION NUMBER: US 60/159,590

PRIOR FILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: US 60/183,322

PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: JP 11-248036

PRIOR FILING DATE: 1999-07-29

PRIOR APPLICATION NUMBER: JP 2000-118776

PRIOR FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: JP 2000-183767

PRIOR FILING DATE: 2000-05-02

PRIOR APPLICATION NUMBER: JP 2000-241899

PRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 35

LENGTH: 1267

TYPE: PRT

ORGANISM: Homo sapiens

US-10-060-065-35

Query Match 47.3%; Score 592.5; DB 14; Length 1267;

Best Local Similarity 47.6%; Pred. No. 5.4e-54;

Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;

Qy 1 QNRDKNYRDLPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60

Db 1018 ENRRKNRYKNLLPYDATRVPLGDEGGYINASFIKIPVCKEEFYIACQGPLTTVGDFWQ 1077

Qy 61 MVLNNCNCVIAITREIECGVVKCYSWPISL-KEPLEFHFVSFLETFHVTQYTVRF 119

Db 1078 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTVSNRLRLALVRMQLKGFVVRAM 1137

Qy 120 QIVKSTGKSCQVHLQTKWPDHGTPTASADFFIKYVRYVRKSHITGPLLHVCAGVGT 179

Db 1138 TLEDIQTREVRHISHLNFTAMPDHTPSQPDLLTFISYMRHHSRGPITHCASAGIRS 1197

Qy 180 GVFIQVDVVSFAIENKNSYFDIMNIVTQMRKQRCGMIOQKEQYFCYEVILEVL 232

Db 1078 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTVSNRLRLALVRMQLKGFVVRAM 1137

Qy 120 QIVKSTGKSCQVHLQTKWPDHGTPTASADFFIKYVRYVRKSHITGPLLHVCAGVGT 179

Db 1138 TLEDIQTREVRHISHLNFTAMPDHTPSQPDLLTFISYMRHHSRGPITHCASAGIRS 1197

Qy 180 GVFIQVDVVSFAIENKNSYFDIMNIVTQMRKQRCGMIOQKEQYFCYEVILEVL 232

Db 1198 GTLICIDVVLGLISQDLDFDISDLVRCMLRQHRGMVQTEDQYIFCYQVILYVL 1250

RESULT 11

US-10-059-585-56

Sequence 56, Application US/10059585

Publication NO. US2003008276A1

GENERAL INFORMATION:

APPLICANT: Saraz, Jan

APPLICANT: Franz, Petra

APPLICANT: Aspenstrm, Pontus

APPLICANT: Hellman, Ulf

APPLICANT: Genez, Leonel Jorge

APPLICANT: Heldin, Carl-Henrik

TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1

GENERAL INFORMATION:

APPLICANT: Ota, Toshio

APPLICANT: Isogai, Takao

APPLICANT: Nishikawa, Tetsuo

APPLICANT: Hayashi, Koji

APPLICANT: Otsuka, Kaoru

APPLICANT: Yamamoto, Jun-ichi

APPLICANT: Ishii, Shizuko

APPLICANT: Sugiyama, Tomoyasu

APPLICANT: Wakamatsu, Ai

APPLICANT: Nagai, Keiichi

APPLICANT: Otsuki, Tetsuji

APPLICANT: Funahashi, Shin-Ichi

APPLICANT: Senoo, Chiaki

APPLICANT: Nezu, Jun-Ichi

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE

FILE REFERENCE: 06501-098001

CURRENT APPLICATION NUMBER: US/10/059,585

CURRENT FILING DATE: 2002-01-29

PRIOR APPLICATION NUMBER: PCT/JP00/05060

PRIOR FILING DATE: 2000-07-28

PRIOR APPLICATION NUMBER: US 60/183,322

PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: US 60/159,590

PRIOR FILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: JP 2000-118776

PRIOR FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: JP 2000-183767

PRIOR FILING DATE: 2000-05-02

PRIOR APPLICATION NUMBER: JP 11-248036

PRIOR FILING DATE: 1999-07-29

NUMBER OF SEQ ID NOS: 64

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 56

LENGTH: 1267

TYPE: PRT

ORGANISM: Homo sapiens

US-10-059-585-56

Query Match 47.3%; Score 592.5; DB 14; Length 1267;

Best Local Similarity 47.6%; Pred. No. 5.4e-54;

Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;

Qy 1 QNRDKNYRDLPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60

Db 1018 ENRRKNRYKNLLPYDATRVPLGDEGGYINASFIKIPVCKEEFYIACQGPLTTVGDFWQ 1077

Qy 61 MVLNNCNCVIAITREIECGVVKCYSWPISL-KEPLEFHFVSFLETFHVTQYTVRF 119

Db 1078 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTVSNRLRLALVRMQLKGFVVRAM 1137

Qy 120 QIVKSTGKSCQVHLQTKWPDHGTPTASADFFIKYVRYVRKSHITGPLLHVCAGVGT 179

Db 1138 TLEDIQTREVRHISHLNFTAMPDHTPSQPDLLTFISYMRHHSRGPITHCASAGIRS 1197

Qy 180 GVFIQVDVVSFAIENKNSYFDIMNIVTQMRKQRCGMIOQKEQYFCYEVILEVL 232

Db 1198 GTLICIDVVLGLISQDLDFDISDLVRCMLRQHRGMVQTEDQYIFCYQVILYVL 1250

RESULT 12

US-10-177-980-12

Sequence 12, Application US/10177980

Publication NO. US20030166232A1

GENERAL INFORMATION:

APPLICANT: Saraz, Jan

APPLICANT: Franz, Petra

APPLICANT: Aspenstrm, Pontus

APPLICANT: Hellman, Ulf

APPLICANT: Genez, Leonel Jorge

APPLICANT: Heldin, Carl-Henrik

TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1

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FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/10/177,980
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/080,855
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 08/805,583
; PRIOR FILING DATE: 1997-02-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 2466
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-177-980-12

Query Match 47.3%; Score 592.5; DB 14; Length 2466;
Best Local Similarity 47.6%; Pred. No. 1.3e-53;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;

QY 1 QNRDKNRYRDLIPYDSTRVPLGKKNKYINASYIRIVNHEEEFYIATQGPLPETIEDFWQ 60
Db 2217 ENRRKNRYKNILPYDATRVPLGDEGGYINASFIPVKGEFVYIACQGPLTTVGDFWQ 2276
QY 61 MVLNNCNVIMTIREICGVKICYSWPISL-KEPLEFHFVSFLETHVTFYTVRVF 119
Db 2277 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTMVSNRLRLALVRMQQLKGFVVRAM 2336
QY 120 QIVKSTGKSCQVKHLQFTKWPDPHGTPASADFFIKYVVRKSHITGPLLHVCAGVGT 179
Db 2337 TLEDIQTREVRHISHLNFTAMPDHDTPSQPDLLTFISYMRHRSGLIITHCSAGIGRS 2396
QY 180 GVFCVDVWVFSAEIKNYSFDIMNIVTQMRKQRCGMIOQKEQYQFCYEIVLEVL 232
Db 2397 GTLICIDVVLGLISQDLDFDISLVRMRLQRHGMVQTEDQYIFCYQVILYVL 2449

RESULT 13
US-10-795-148-2
; Sequence 2, Application US/10795148
; Publication No. US20040224337A1
; GENERAL INFORMATION:
; APPLICANT: FOHR, ERIK
; APPLICANT: JERICIC, JASNA
; APPLICANT: LORENTE, GUSTAVO A.
; APPLICANT: UFRER, ROMAN
; TITLE OF INVENTION: USE OF BIOMOLECULAR TARGETS IN THE
; TREATMENT AND VISUALIZATION OF TUMORS
; FILE REFERENCE: AGYT-022
; CURRENT APPLICATION NUMBER: US/10/795,148
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/452,169
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2466
; TYPE: PRF
; ORGANISM: H. sapiens
US-10-795-148-2

Query Match 47.3%; Score 592.5; DB 17; Length 2466;
Best Local Similarity 47.6%; Pred. No. 1.3e-53;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;

QY 1 QNRDKNRYRDLIPYDSTRVPLGKKNKYINASYIRIVNHEEEFYIATQGPLPETIEDFWQ 60
Db 2217 ENRRKNRYKNILPYDATRVPLGDEGGYINASFIPVKGEFVYIACQGPLTTVGDFWQ 2276
QY 61 MVLNNCNVIMTIREICGVKICYSWPISL-KEPLEFHFVSFLETHVTFYTVRVF 119
Db 2277 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTMVSNRLRLALVRMQQLKGFVVRAM 2336
QY 120 QIVKSTGKSCQVKHLQFTKWPDPHGTPASADFFIKYVVRKSHITGPLLHVCAGVGT 179
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FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/10/177,980
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/080,855
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 08/805,583
; PRIOR FILING DATE: 1997-02-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 2466
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-177-980-12

Query Match 47.3%; Score 592.5; DB 9; Length 2485;
Best Local Similarity 47.6%; Pred. No. 1.3e-53;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;

QY 1 QNRDKNRYRDLIPYDSTRVPLGKKNKYINASYIRIVNHEEEFYIATQGPLPETIEDFWQ 60
Db 2236 ENRRKNRYKNILPYDATRVPLGDEGGYINASFIPVKGEFVYIACQGPLTTVGDFWQ 2295
QY 61 MVLNNCNVIMTIREICGVKICYSWPISL-KEPLEFHFVSFLETHVTFYTVRVF 119
Db 2296 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTMVSNRLRLALVRMQQLKGFVVRAM 2355
QY 120 QIVKSTGKSCQVKHLQFTKWPDPHGTPASADFFIKYVVRKSHITGPLLHVCAGVGT 179
Db 2356 TLEDIQTREVRHISHLNFTAMPDHDTPSQPDLLTFISYMRHRSGLIITHCSAGIGRS 2415
QY 180 GVFCVDVWVFSAEIKNYSFDIMNIVTQMRKQRCGMIOQKEQYQFCYEIVLEVL 232
Db 2416 GTLICIDVVLGLISQDLDFDISLVRMRLQRHGMVQTEDQYIFCYQVILYVL 2468

RESULT 15
US-10-619-220-46
; Sequence 46, Application US/10619220
; Publication No. US20040033979A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/10/619,220
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 09/802,669
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
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Wed Dec 1 14:18:27 2004

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; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 2485
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-619-220-46

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Query Match	47.3%;	Score 592.5;	DB 15;	Length 2485;
Best Local Similarity	47.6%;	Pred.No.1.3e-53;		
Matches 111;	Conservative 41;	Mismatches 80;	Indels 1;	Gaps 1;
QY	1	QNRKRNRYDILPYDSTRVPLGKNKDYNINASYRIVNHEEYFYIATQGPLTETDFWQ	60	
Db	2236	ENRRKRNRYKNLLPYDATRVPLDGEGGYINASFKIPVGKEEFYIACQGLEPTTVGDWFQ	2295	
QY	61	MVLNNCNCVIAMITRIECGVIKCYSWPISI--KEPLEFEHFSVFLETFHVTQYFVRVF	119	
Db	2296	MIWEQKSTVIAMTTOVEGEKIKCRQYWNLIGKTTMNSRLRALVRMQLGKGFVRAM	2355	
QY	120	QIVKKSSTGSKQCVKHLQFTKPDHGTPASADPFKIYRVYVRKSHITGLPLVHCSSAGVRT	179	
Db	2356	TLEDIQTRVRRHISHLNTAWPDHPDTSPDDLLLTFSYMRHHTHRSGPIITHCSAGIRS	2415	
QY	180	GVPICVDVFPISALEKNYSFDIMNIIVTMQRKORCGMIQTKEQYFCYEIVLEV	232	
Db	2416	GTLCIDHWLGLSLSQLDELDSOLVRCMLQRHGVMQTEQDYIFCFQVILIYL	2468	

Search completed: December 1, 2004, 12:52:38
Job time : 425.441 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	592.5	47.3	2465	2	US-08-596-291-3	Sequence 3, Appli
2	592.5	47.3	2465	3	US-09-100-801-3	Sequence 3, Appli
3	592.5	47.3	2466	3	US-09-080-855-12	Sequence 12, Appl
4	592.5	47.3	2466	4	US-09-566-076-12	Sequence 12, Appl
5	592.5	47.3	2466	5	PCF-US94-09943-2	Sequence 2, Appli
6	592.5	47.3	2485	5	US-09-290-640-46	Sequence 46, Appl
7	592.5	47.3	2485	4	US-09-665-615B-46	Sequence 46, Appl
8	499	39.8	913	4	US-09-848-294-2	Sequence 2, Appli
9	489	39.4	231	4	US-09-848-294-7	Sequence 7, Appli
10	494	39.0	244	2	US-08-446-345-37	Sequence 37, Appl
11	487	38.9	242	2	US-08-685-992-21	Sequence 21, Appl
12	487	38.9	242	2	US-09-144-925-21	Sequence 21, Appl
13	483.5	38.6	1911	1	US-08-348-008B-5	Sequence 5, Appli
14	483.5	38.6	1911	2	US-08-800-825A-5	Sequence 5, Appli
15	483.5	38.6	1911	3	US-09-158-657-5	Sequence 5, Appli
16	483.5	38.6	1911	5	PCF-US94-10166-5	Sequence 5, Appli
17	476.5	38.0	278	1	US-08-201-697-16	Sequence 16, Appl
18	475	37.9	1337	3	US-08-854-585-2	Sequence 2, Appli
19	475	37.9	1337	4	US-09-447-533-2	Sequence 2, Appli
20	475	37.9	1337	5	PCF-US95-05512-2	Sequence 2, Appli
21	474.5	37.9	1501	2	US-08-447-464-3	Sequence 3, Appli
22	474.5	37.9	1501	2	US-08-716-679-3	Sequence 3, Appli
23	468	37.4	1457	2	US-08-652-971-3	Sequence 3, Appli
24	468	37.4	1457	2	US-08-449-644-1	Sequence 3, Appli
25	468	37.4	1457	2	US-08-087-244A-1	Sequence 1, Appli
26	468	37.4	1457	2	US-08-991-258A-3	Sequence 1, Appli
27	468	37.4	1457	2	US-08-769-399-3	Sequence 3, Appli

Query Match	47.3%	Score 592.5;	DB 2;	Length 2465;
Best Local Similarity	47.6%;	Pred. No. 1.2e-50;		

Matches	111;	Conservative	41;	Mismatches	80;	Indels	1;	Gaps	1;
Qy	1	QNRDKRVRDILPYDSTRVPLGKNDYINASVIRIVNHEEVEFYIATQGPLPETIEDFWQ	60						
Db	2216	ENRRKRYKNILPYDSTRVPLGDEGYINASIKIPVGKEEFYIACQGPLPTTVGDFWQ	2275						
Qy	61	MYLENNCNVIAMITREICGVIKCYSWPFISL-KEPLEPEHSPSVFLETHVTQYFVVRVF	119						
Db	2276	MIWEQKSTVIAMMTQVEGEKIKCQRYWENILGKTTMVSNNRULALVRMQLKGFFVVRAM	2335						
Qy	120	QIVKSGTKSCQVKHLQFTKWDPHGTPAGADFFIKVRYVRVKSHITGPLLVHCSAGVGT	179						
Db	2336	TLEDICTREVRHLSHLFTAWPDHDTSPQDDLLTFISYMRHITHRSGPIITHCSAGIGRS	2395						
Qy	180	GVFIQVDVVVFSALREKNYSFDIMNIIVTQMRKQRCMIQTKEOYQCFVEIVLEVL	232						
Db	2396	GTLCIDVVLGLISDLDDELISQVRCMRQLRHGMVQTEQDYIFCQVILVYL	2448						

RESULT 2

US-09-100-804-3
Sequence 3, Application US/09100804
Patent No. 6066472
GENERAL INFORMATION:
APPLICANT: GONEZ, LEONEL JORGE
APPLICANT: SARAS, JAN
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONALITY OF NUCLEOTIDE SEQUENCES
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSER: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,804
FILING DATE:

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/100,804
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/596,291
 FILING DATE: 09-AUG-1996
 APPLICATION NUMBER: US 08/115,573
 FILING DATE: 01-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/09943
 FILING DATE: 01-SEP-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: GATES, EDWARD R.
 REGISTRATION NUMBER: 31,616
 REFERENCE/DOCKET NUMBER: LQ461/7003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441
 TELEX:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2465 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-100-804-3

SEQUENCE CHARACTERISTICS:

LENGTH: 2465 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
09-100-804-3

Query Match

```
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Hellman, Ulf
; APPLICANT: Genez, Leonel Jorge
; APPLICANT: Heidin, Carl-Henrik
; TITLE OF INVENTION: PARC, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
; FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/09/566,076
; CURRENT FILING DATE:
; EARLIER APPLICATION NUMBER: 09/080,855
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 2466
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-566-076-12

Query Match          47.3%; Score 592.5; DB 4; Length 2466;
Best Local Similarity 47.6%; Pred. No. 1.2e-60;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;

QY 1 QNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIWNHEEYFYIATQGPLPETIEDFWQ 60
Db 2217 ENRRKNRYKNILPYDATRVPLGDEGGYINASFIPKIPVGKEEFYIACQGPLPTTVGDFWQ 2276
QY 61 MVLENNCNVIAMITREIECGVIKCYSWPISL-KEPLEFEHFSVFLETHVTOYFTVRVF 119
Db 2277 MIWEQKSTVIAMMTQVEGEKIKCQRYWPNILGKTTMVSNNRLALVRMQQLKGFVVRAM 2336
QY 120 QIVKSTGSKSQCVKHLQFTKWPDHGTPASADFFIKVYRVYRKSHITGPLLHCSAGVGT 179
Db 2337 TLEDIQTREVRHISHLNFTAWPDHPTSPQDLDLTFISYMRHHSRGPITTHCSAGIGRS 2396
QY 180 GVFCVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOQKEQYFCYVEIVLEVL 232
Db 2397 GTLICIDVVLGLISQDLDFDISLVRCLQRHGMVQTEDQYIFCYQVILYVL 2449

RESULT 5
PCT-US94-09943-2
; Sequence 2, Application PC/TUS9409943
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09943
; FILING DATE: 01-SEP-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/115,573
; FILING DATE: 01-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: TWOMEY, MICHAEL J.
; REGISTRATION NUMBER: P-38,349
; REFERENCE/DOCKET NUMBER: L0461/7000WO
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; TELEX: 92-1742 EZBKIEL
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2466 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
PCT-US94-09943-2

Query Match          47.3%; Score 592.5; DB 5; Length 2466;
Best Local Similarity 47.6%; Pred. No. 1.2e-60;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;

QY 1 QNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIWNHEEYFYIATQGPLPETIEDFWQ 60
Db 2217 ENRRKNRYKNILPYDATRVPLGDEGGYINASFIPKIPVGKEEFYIACQGPLPTTVGDFWQ 2276
QY 61 MVLENNCNVIAMITREIECGVIKCYSWPISL-KEPLEFEHFSVFLETHVTOYFTVRVF 119
Db 2277 MIWEQKSTVIAMMTQVEGEKIKCQRYWPNILGKTTMVSNNRLALVRMQQLKGFVVRAM 2336
QY 120 QIVKSTGSKSQCVKHLQFTKWPDHGTPASADFFIKVYRVYRKSHITGPLLHCSAGVGT 179
Db 2337 TLEDIQTREVRHISHLNFTAWPDHPTSPQDLDLTFISYMRHHSRGPITTHCSAGIGRS 2396
QY 180 GVFCVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOQKEQYFCYVEIVLEVL 232
Db 2397 GTLICIDVVLGLISQDLDFDISLVRCLQRHGMVQTEDQYIFCYQVILYVL 2449

RESULT 6
US-09-290-640-46
; Sequence 46, Application US/09290640
; Patent No. 6204055
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0351
; CURRENT APPLICATION NUMBER: US/09/290,640
; CURRENT FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 2485
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-290-640-46

Query Match          47.3%; Score 592.5; DB 3; Length 2485;
Best Local Similarity 47.6%; Pred. No. 1.2e-60;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;

QY 1 QNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIWNHEEYFYIATQGPLPETIEDFWQ 60
Db 2236 ENRRKNRYKNILPYDATRVPLGDEGGYINASFIPKIPVGKEEFYIACQGPLPTTVGDFWQ 2295
QY 61 MVLENNCNVIAMITREIECGVIKCYSWPISL-KEPLEFEHFSVFLETHVTOYFTVRVF 119
Db 2296 MIWEQKSTVIAMMTQVEGEKIKCQRYWPNILGKTTMVSNNRLALVRMQQLKGFVVRAM 2355
QY 120 QIVKSTGSKSQCVKHLQFTKWPDHGTPASADFFIKVYRVYRKSHITGPLLHCSAGVGT 179
Db 2356 TLEDIQTREVRHISHLNFTAWPDHPTSPQDLDLTFISYMRHHSRGPITTHCSAGIGRS 2415
QY 180 GVFCVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOQKEQYFCYVEIVLEVL 232
Db 2416 GTLICIDVVLGLISQDLDFDISLVRCLQRHGMVQTEDQYIFCYQVILYVL 2468
```

```

Query Match      39.8%; Score 499; DB 4; Length 913;
Best Local Similarity 42.0%; Pred. No. 3.7e-50;
Matches 102; Conservative 38; Mismatches 85; Indels 18; Gaps 5;

QY 1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYI-----RIVNHEEYFYIATQGLPE 53
Db 669 QNLDKNRYKDVLPYDTRVLQGNEDYINASYVMEIPAANLVNK-----YIATQGLPH 723
QY 54 TIEFQWVLENNCNVIAITREIEGCVIKCYSWPISLKEPLEFEH--FSVLETFHVT 111
Db 724 TCAQFWQVVDOKLSLIVMLTTLTERGRYKCHQYWP---DPPDVNHHGGFHIQCQSEDCT 780
QY 112 QYFTVRVFOIVKSTGKSCQVKHLQFTKWPDHGTSPASADFFIKYVYVRKSHI-TGPLL 170
Db 781 IAVSRMLVTNTQTGEEHTVTHLQVAMPDHGIPDDSDFLFVNYVRSRLVDSPEVLV 840
QY 171 HCSAGVGTGVFICVDVVSFAIEKNYSFDIMNVTQMRKQRCGMICQYQCYEIVLE 230
Db 841 HCSAGIGRTGVLTMETAMCLTERNLPIYPLDIVRKMRDORAMMVOTSSQYKFVCEAILR 900
QY 231 VLQ 233
Db 901 VYE 903

RESULT 9
US-09-848-294-7
; Sequence 7, Application US/09848294
; Patent No. 6479640
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el
; TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal
; TITLE OF INVENTION: Adhesions and Uses Therefor
; FILE REFERENCE: CSHL90-04FZA
; CURRENT APPLICATION NUMBER: US/09/848,294
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 09/235,251
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 08/759,536
; PRIOR FILING DATE: 1996-12-04
; PRIOR APPLICATION NUMBER: 08/107,420
; PRIOR FILING DATE: 1993-08-16
; PRIOR APPLICATION NUMBER: 07/663,579
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 07/494,036
; PRIOR FILING DATE: 1990-03-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homosapiens
US-09-848-294-7

Query Match      39.4%; Score 494; DB 4; Length 244;
Best Local Similarity 41.7%; Pred. No. 2.2e-50;
Matches 101; Conservative 38; Mismatches 85; Indels 18; Gaps 5;

QY 2 NRDKNRYRDILPYDSTRVPLGKNKDYINASYI-----RIVNHEEYFYIATQGLPET 54
Db 1 NLDKNRYKDVLPYDTRVLQGNEDYINASYVMEIPAANLVNK-----YIATQGLPHT 55
QY 55 IEDFQWVLENNCNVIAITREIEGCVIKCYSWPISLKEPLEFEH--FSVLETFHVTQ 112
Db 56 CAQFWQVVDOKLSLIVMLTTLTERGRYKCHQYWP---DPPDVNHHGGFHIQCQSEDCTI 112
QY 113 YFTVRVFOIVKSTGKSCQVKHLQFTKWPDHGTSPASADFFIKYVYVRKSHI-TGPLL 171
Db 113 AVSRMLVTNTQTGEEHTVTHLQVAMPDHGIPDDSDFLFVNYVRSRLVDSPEVLV 172
QY 172 CSAGVGTGVFICVDVVSFAIEKNYSFDIMNVTQMRKQRCGMICQYQCYEIVLE 231
Db 172 CSAGVGTGVFICVDVVSFAIEKNYSFDIMNVTQMRKQRCGMICQYQCYEIVLE 231
```

```

Query Match      47.3%; Score 592.5; DB 4; Length 2485;
Best Local Similarity 47.6%; Pred. No. 1.2e-60;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;

QY 1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGLPETIEDFWQ 60
Db 2236 ENRRKNRYKNILPYDATRVPLGDBGGYINAFIKIPVGKEEFVYIACQGLPTTVGDFWQ 2295
QY 61 MVLENNCNVIAITREIEGCVIKCYSWPISL-KEPLEFEHFSVLETFHVTQYFTVRVF 119
Db 2296 MIWEQSTVIAMTQVEGEKIKQRYWPNILGKTTWNSRLRLVARMQQLKGFVVVRAM 2355
QY 120 QIVKSTGKSCQVKHLQFTKWPDHGTSPASADFFIKYVYVRKSHITGPLLHCSAGVGR 179
Db 2356 TLEDIQTRVHRHSHLNTAWPDHDTSPQDDLLTFISYMRHHRSGPIITHCSAGIGRS 2415
QY 180 GVFIQVDVVSFAIEKNYSFDIMNVTQMRKQRCGMICQYQCYEIVLEVL 232
Db 2416 GTLICIDVVLGISQDLDFDISDLVRCMLQRHGMVQTDQYIFCYQVILYVL 2468

RESULT 8
US-09-848-294-2
; Sequence 2, Application US/09848294
; Patent No. 6479640
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el
; TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal
; TITLE OF INVENTION: Adhesions and Uses Therefor
; FILE REFERENCE: CSHL90-04FZA
; CURRENT APPLICATION NUMBER: US/09/848,294
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 09/235,251
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 08/759,536
; PRIOR FILING DATE: 1996-12-04
; PRIOR APPLICATION NUMBER: 08/107,420
; PRIOR FILING DATE: 1993-08-16
; PRIOR APPLICATION NUMBER: 07/663,579
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 07/494,036
; PRIOR FILING DATE: 1990-03-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 913
; TYPE: PRT
; ORGANISM: Homosapiens
US-09-848-294-2
```

Db 173 CSAGIGRTGLVMTAMCLTERNLPIYPLDIVKMRDQRAMMVQTSQYKFVCEAILRV 232

Qy 232 LQ 233

Db 233 YE 234

RESULT 10

US-08-446-345-37

Sequence 37, Application US/08446345

Patent No. 5831009

GENERAL INFORMATION:

APPLICANT: Ullrich, Axel

APPLICANT: Moller, Niels P.H.

APPLICANT: Moller, Karin B.

TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE

TITLE OF INVENTION: PHOSPHATASES PTP-D1

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: N.Y.

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,345

FILING DATE: 22-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/234,440

FILING DATE: 28-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30742

REFERENCE/DOCKET NUMBER: 7683-054

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)790-9090

TELEFAX: (212) 869-8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 231 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-446-345-37

Query Match 39.08; Score 489; DB 2; Length 231;

Best Local Similarity 42.08; Pred. No. 7.8e-50;

Matches 100; Conservative 37; Mismatches 83; Indels 18; Gaps 5;

Qy 2 NRDKNRYRDLIPYDSTRVPLGKNDYINASYI-----RIVNHEEYFYIATQGPLPET 54

Db 1 NLDKNRYKDVLPYDTRVLVLLQGNEDYINASYVNMIEIPAANLVNK-----YIATQGPLPHT 55

Qy 55 IEDFWQVLENNCNVMIATREIECGVKYKSYWPISLKEPFLPEFH--FSVFLTFHTQ 112

Db 56 CAQFWQVWVDQKLSLVMLTLTTERGRTKCHQWP---DPPDVNMHGGFIQCQSDCTI 112

Qy 113 YFTVRVRFQ--IVKSKTGSKQCVKHLQFTKWPDHGTPASADFFIKYRVYRKSHI--TGPLLVH 171

Db 113 AYSREMLVTNTQTGEHTVTHLQYVAVPDHGIPTDSSDFLEFVNYVRSRLRVDSEPLVH 172

Qy 172 CSAGVGRGTGVICVDVWVFAIEKNYSFDIMNIVTOMRKORCGMIQTKEQYQFCYEV 229

Db 173 CSAGIGRTGLVMTAMCLTERNLPIYPLDIVKMRDQRAMMVQTSQYKFVCEAIL 230

RESULT 11

US-08-685-992-21

Sequence 21, Application US/08685992

Patent No. 5912138

GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas

APPLICANT: Flint, Andrew J.

TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN

TITLE OF INVENTION: TYROSINE PHOSPHATASES

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/685,992

FILING DATE: 25-JUL-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: CSHL96-03

TELECOMMUNICATION INFORMATION:

TELEPHONE: 781-861-6240

TELEFAX: 781-861-9540

TELEX:

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 242 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-685-992-21

Query Match 38.98; Score 487; DB 2; Length 242;

Best Local Similarity 41.88; Pred. No. 1.4e-49;

Matches 102; Conservative 37; Mismatches 79; Indels 26; Gaps 7;

Qy 1 QNRDKNRYRDLIPYDSTRVPLGKNDYINASYI-----RIVNHEEYFYIATQGPLPE 53

Db 11 QNLDKNRYKDVLPYDTRVLVLLQGNEDYINASYVNMIEIPAANLVNK-----YIATQGPLPH 65

Qy 54 TIEDFWQVLENNCNVMIATREIECGVKYKSYWPISLKEPFLPEFHFSVFLTFHTV--- 110

Db 66 TCAQFWQVWVDQKLSLVMLTLTTERGRTKCHQWP---DPPDVNMHGG-----FHIQCQ 117

Qy 111 TQFTVRVFO--IVKSKTGSKQCVKHLQFTKWPDHGTPASADFFIKYRVYRKSHI--TGP 167

Db 118 SECTAIYVSMVLTNTQTGEHTVTHLQYVAVPDHGIPTDSSDFLEFVNYVRSRLRVDSEP 177

Qy 168 LLVHCSAGVGRGTGVICVDVWVFAIEKNYSFDIMNIVTOMRKORCGMIQTKEQYQFCYEI 227

Db 178 VLHCSAGIGRTGLVMTAMCLTERNLPIYPLDIVKMRDQRAMMVQTSQYKFVCEA 237

Qy 228 VLEV 231

Db 238 ILRV 241

RESULT 12

US-09-144-925-21
 ; Sequence 21, Application US/09144925
 ; Patent No. 5951979
 ; GENERAL INFORMATION:
 ; APPLICANT: Tonks, Nicholas
 ; APPLICANT: Flint, Andrew J.
 ; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
 ; TITLE OF INVENTION: TYROSINE PHOSPHATASES
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02421-4799

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FASTSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/144,925
 FILING DATE:

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/685,992
 FILING DATE: July 25, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: CSHL96-03Z
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 781-861-6240
 TELEFAX: 781-861-9540
 TELEX:

INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 242 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-144-925-21

Query Match 38.9%; Score 487; DB 2; Length 242;
 Best Local Similarity 41.8%; Pred. No. 1.4e-49;
 Matches 102; Conservative 37; Mismatches 79; Indels 26; Gaps 7;

QY 1 QNRDKNRYRDLPLDSTRTVPLGKNKDYINASYI-----RIVNHEEYFYIATQGLPLPE 53
 DB 11 QNLDKNRYKDYLPYDTTTRVLLQGNEDYINASYVNMIEIPANLVNK-----VIATQGLPLPH 65
 QY 54 TIEDPQWMLNCCNVIAMITREIBCGVIKCVSYMPISLKEPLEPEHFSVLETHPV--- 110
 DB 66 TCAQFQWVWQKLSLIVMLTLTRGRKTKHQWP---DPDVMNHGG-----PHICQ 117
 QY 111 TQYTFVTRVFO--IVKSTGKSCQVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHI-TGP 167
 DB 118 SEDCTIAYVSMVINTQGEETHVTTHLQVAMPDHGIPDDSSDFLEFVNYVRSRLVDSEP 177
 QY 168 LIVHCSAGVGTGVFICVDVVFSALEKNVSPDIMNIVTMQRKQRCGMIOQKEQYQFCVEI 227
 DB 178 VLVHCSAGIGRTGVLTVMETAMCLTERNLPIYPLDVIVRKMRDQRAMVQTSSQYKVFCEA 237
 QY 228 VLEV 231
 DB 238 ILRV 241

RESULT 13

US-08-348-006B-5

; Sequence 5, Application US/08348006B
 ; Patent No. 5658756
 ; GENERAL INFORMATION:
 ; APPLICANT: RODAN, GIDEON A.
 ; APPLICANT: RUTLEDGE, AZRIEL
 ; TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
 ; TITLE OF INVENTION: TYROSINE PHOSPHATASE
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: J. MARK HAND
 ; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
 ; CITY: RAHWAY
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07065-0900

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/348,006B
 FILING DATE:

CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/122,032
 FILING DATE: 14-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: HAND, J., MARK
 REGISTRATION NUMBER: 36,545
 REFERENCE/DOCKET NUMBER: 189921A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 908-594-3905
 TELEFAX: 908-594-4720
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1911 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-348-006B-5

Query Match 38.6%; Score 483.5; DB 1; Length 1911;
 Best Local Similarity 42.0%; Pred. No. 7.7e-48;
 Matches 100; Conservative 44; Mismatches 79; Indels 15; Gaps 6;

QY 5 KNRYRDILPYDSTRVPLG-----KNKDYINASYIRIVNHEEYFYIATQGLPETIEDFW 59
 DB 1671 KNRLVNIMPYESTRVCLQPIRGVSGDYINASFID--GYRQOKAYIATQGLAETEDFW 1728
 QY 60 QMVLNCCNVIAMITREIBCGVIKCVSYMPISLKEPLEPEHFSVFLTEFHTQYFTVRV 118
 DB 1729 RMLWENNSTIVVMLTKUREMGRKCHQWP--AERSARYQIVVDPMAYNMQYI-LRE 1785
 QY 119 FOIVKSTGKSCQVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHI-----ITGPLLHCSA 174
 DB 1796 FKVTARDARQGSRTVRQFQFTDWPQGVKPSGEGFIDFGVHKTKQFGQGPISVHCSA 1845
 QY 175 GVGRGTGVFICVDVVFSALEKNVSPDIMNIVTMQRKQRCGMIOQKEQYQFCVEI 232
 DB 1846 GVGRGTGVFITLSILERMRYEGVVDIFQTVKMLRTQRPAMYQTEDEYQFCQAALLEYL 1903

RESULT 14

US-08-800-825A-5
 ; Sequence 5, Application US/08800825A
 ; Patent No. 5866397
 ; GENERAL INFORMATION:
 ; APPLICANT: RODAN, GIDEON A.
 ; APPLICANT: SCHMIDT, AZRIEL
 ; APPLICANT: RUTLEDGE, SU JANE

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 1, 2004, 12:07:39 ; Search time 81.7544 Seconds
(without alignments)
1022.379 Million cell updates/sec

Title: US-09-095-478A-6_COPY_225_457

Perfect score: 1253

Sequence: 1 QNRDKNRYRDIILPYDSTRVP.....MIQTKEQYQFCYEVIVLEVLQ 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1253	100.0	426	2	AAW89249 Mouse PTP
2	1253	100.0	463	2	AAW89250 Mouse PTP
3	1174	93.7	405	2	AAW89251 Mouse PTP
4	1003	80.0	261	6	AAE37994 Human kin
5	1003	80.0	420	5	AAE14454 Human pro
6	995	78.4	398	5	ABG30845 Human tyr
7	995	79.4	398	7	ADD89795 Human DKE
8	995	79.4	409	7	AD809123 Novel pro
9	995	79.4	508	7	AD808106 Novel pro
10	995	79.4	561	4	ABG06042 Novel hum
11	941	75.1	412	6	AAE37996 Human kin
12	639	51.0	348	8	ADK71863 Human kin
13	592.5	47.3	766	6	ABU70688 Human adi
14	592.5	47.3	1267	4	AAE67637 Amino aci
15	592.5	47.3	1267	4	AAE67637 Amino aci
16	592.5	47.3	2466	2	AAE71498 Human pro
17	592.5	47.3	2466	2	AAW75999 Intracell
18	592.5	47.3	2466	3	AAE90272 Human PTP
19	592.5	47.3	2485	3	AAE19343 Amino aci
20	592.5	47.3	2485	7	ADJ69543 Human hea
21	592.5	47.3	2485	8	ADL27685 Human Fas
22	592.5	47.3	2485	8	ADM53457 Human Fas
23	566	45.2	122	2	AAW89252 Rat PTP10
24	538	42.9	235	5	ADI17283 Polypepti
25	514	41.0	1028	8	ADF43232 Mouse PTP

ALIGNMENTS

RESULT 1
AAW89249
ID AAW89249 standard; protein; 426 AA.
XX
AC AAW89249;
XX
DT 10-MAR-1999 (first entry)
XX
DE Mouse PTP05.
XX
KW PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;
KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;
KW neurodegenerative disease; neuronal survival; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease.
XX
OS Mus sp.
XX
PN WO9849317-A2.
XX
PD 05-NOV-1998.
XX
PF 27-APR-1998; 98WO-US008439.
XX
PR 28-APR-1997; 97US-0044428P.
PR 20-MAY-1997; 97US-0047222P.
PR 11-JUN-1997; 97US-0049477P.
PR 11-JUN-1997; 97US-0049756P.
PR 18-JUN-1997; 97US-0049914P.
PR 23-OCT-1997; 97US-0063595P.
XX
(SUGEN) SUGEN INC.
XX
PI Plowman GB, Clary D, Jallal B, Peles E, Onrust S, Markby D;
PI Courtneidge SA, App H, Hui TH;
XX
DR WPI; 1999-009434/01.
DR N-PSDB; AAW81744.
XX
New nucleic acid encoding specific protein tyrosine phosphatases - useful
for identifying specific modulators for treatment and prevention of
cancer and neurodegenerative disease.
Claim 2; Page 155-157; 193pp; English.
The present invention describes isolated, enriched or purified nucleic
acids encoding PTP04, SAD, PTP05, ALP and ALK-7 proteins. The
present sequence represents mouse PTP05. The above proteins, other than
ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify

26 500 39.9 913 8 ADO55173
27 499 39.8 868 8 ADF43234 Human PTP
28 499 39.8 913 2 AAW12522
29 499 39.8 913 2 AAW25156 Human PTP
30 499 39.8 913 5 AAG79333
31 499 39.8 913 7 ADD22982
32 499 39.8 913 7 ADL16189 Human pro
33 499 39.8 913 8 ADF43230 Human PTP
34 488.5 39.0 1948 7 ADD18742 Human dis
35 488.5 39.0 1949 7 ADE57117 Human pro
36 488.5 39.0 1949 7 ADE57121 Human pro
37 488.5 39.0 1949 7 ADD47019 Human pro
38 488.5 39.0 1949 7 ADD47015 Human pro
39 488 38.9 703 7 ADL16191 Human pro
40 487 38.9 291 4 AAG78282 Human PTP
41 483.5 38.6 1911 2 AAR71726 Human PTP
42 483.5 38.6 1911 2 AAW27225 Human PTP
43 483.5 38.6 1911 2 AAW94027 Human pro
44 483.5 38.6 1911 4 AAU01459 Human pro
45 482.5 38.5 1254 8 ADN02662 Liver dis

CC substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; CC to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the proteins

XX Sequence 426 AA;
SQ Query Match 100.0%; Score 1253; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 7.8e-136; Indels 0; Gaps 0;
Matches 233; Conservative 0; Mismatches 0;
QY 1 QNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
DB 188 QNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 247
QY 61 MVLENNCNVIAITREIEGVIKCYSWPISLKEPLEFHSVFLTEHVTQYFTVRVQ 120
DB 248 MVLENNCNVIAITREIEGVIKCYSWPISLKEPLEFHSVFLTEHVTQYFTVRVQ 307
QY 121 IVKSTGKSCQVXHLQFTKWPDHGTPASADFFIKYVYVRKSHITGPLLHVCSAGVGRGTG 180
DB 308 IVKSTGKSCQVXHLQFTKWPDHGTPASADFFIKYVYVRKSHITGPLLHVCSAGVGRGTG 367
QY 181 VFICVDVWFSIAIEKNYSFDMINIVTQMRKQRCGMIQTKQYQFCYEIVLEVLQ 233
DB 368 VFICVDVWFSIAIEKNYSFDMINIVTQMRKQRCGMIQTKQYQFCYEIVLEVLQ 420

RESULT 2
AAW89250
ID AAW89250 standard; protein; 463 AA.
XX AC AAW89250;
XX DT 10-MAR-1999 (first entry)
XX DE Mouse PTP05 isoform #1.
XX PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;
KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;
KW neurodegenerative disease; neuronal survival; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease.
XX OS Mus sp.
XX PN WO9849317-A2.
XX PD 05-NOV-1998.
XX PF 27-APR-1998; 98WO-US008439.
XX PR 28-APR-1997; 97US-0044428P.
XX PR 20-MAY-1997; 97US-0047222P.
XX PR 11-JUN-1997; 97US-0049477P.
XX PR 11-JUN-1997; 97US-0049756P.
XX PR 18-JUN-1997; 97US-0049914P.
XX PR 23-OCT-1997; 97US-0063595P.
XX PA (SUGEN-) SUGEN INC.
XX PI Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;
PI Courtneidge SA, App H, Hui TH;
XX WPI; 1999-009434/01.
XX N-PSDB; AAW81745.

XX New nucleic acid encoding specific protein tyrosine phosphatases - useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.

XX Claim 2; Page 157-158; 193pp; English.

XX The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The present sequence represents mouse PTP05. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; CC to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the proteins

XX Sequence 463 AA;
SQ Query Match 100.0%; Score 1253; DB 2; Length 463;
Best Local Similarity 100.0%; Pred. No. 8.8e-136; Indels 0; Gaps 0;
Matches 233; Conservative 0; Mismatches 0;
QY 1 QNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
DB 225 QNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 284
QY 61 MVLENNCNVIAITREIEGVIKCYSWPISLKEPLEFHSVFLTEHVTQYFTVRVQ 120
DB 285 MVLENNCNVIAITREIEGVIKCYSWPISLKEPLEFHSVFLTEHVTQYFTVRVQ 344
QY 121 IVKSTGKSCQVXHLQFTKWPDHGTPASADFFIKYVYVRKSHITGPLLHVCSAGVGRGTG 180
DB 345 IVKSTGKSCQVXHLQFTKWPDHGTPASADFFIKYVYVRKSHITGPLLHVCSAGVGRGTG 404
QY 181 VFICVDVWFSIAIEKNYSFDMINIVTQMRKQRCGMIQTKQYQFCYEIVLEVLQ 233
DB 405 VFICVDVWFSIAIEKNYSFDMINIVTQMRKQRCGMIQTKQYQFCYEIVLEVLQ 457

RESULT 3
AAW89251
ID AAW89251 standard; protein; 405 AA.
XX AC AAW89251;
XX DT 10-MAR-1999 (first entry)
XX DE Mouse PTP05 isoform #2.
XX PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;
KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;
KW neurodegenerative disease; neuronal survival; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease.
XX OS Mus sp.
XX PN WO9849317-A2.
XX PD 05-NOV-1998.
XX PF 27-APR-1998; 98WO-US008439.
XX PR 28-APR-1997; 97US-0044428P.
XX PR 20-MAY-1997; 97US-0047222P.
XX PR 11-JUN-1997; 97US-0049477P.

PR 11-JUN-1997; 97US-0049756P.
 PR 18-JUN-1997; 97US-0049914P.
 PR 23-OCT-1997; 97US-0063595P.
 XX (SUGEN-) SUGEN INC.
 XX Plowman GD, Clary D, Jallai B, Peles E, Onrust S, Markby D;
 PI Courtneidge SA, App H, Hui TH;
 XX WPI; 1999-009434/01.
 DR N-PSDB; AAV81746.
 XX
 PT New nucleic acid encoding specific protein tyrosine phosphatases - useful
 PT for identifying specific modulators for treatment and prevention of
 PT cancer and neurodegenerative disease.
 XX
 PS Claim 2; Page 158-160; 193pp; English.
 XX The present invention describes isolated, enriched or purified nucleic
 CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The
 CC present sequence represents mouse PTP05. The above proteins, other than
 CC ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify
 CC substances that modulate their activity (i.e. agonists and antagonists,
 CC including NBP) in vivo or in vitro. These substances are used to treat or
 CC prevent diseases associated with abnormal signal transduction pathways
 CC that involve the proteins, particularly cancer (e.g. leukaemia and
 CC lymphoma), while modulators of ALK-7 (which is a type I receptor
 CC serine/threonine kinase) are used to promote neuronal survival,
 CC particularly for treating Alzheimer's, Parkinson's or Huntington's
 CC diseases. Nucleic acid fragments of the polynucleotides encoding the
 CC proteins can be used as probes to identify and clone related sequences;
 CC to detect protein-encoded RNA; to generate transgenic animals and in gene
 CC therapy (optionally after mutation). Ab are used to determine the
 CC proteins
 XX
 SQ Sequence 405 AA;
 Query Match 93.7%; Score 1174; DB 2; Length 405;
 Best Local Similarity 100.0%; Pred. No. 1e-126;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QNRDKNRYDILPYDSTRVPLGKNDKYNINASYIRIVNHEEYFYIATQGLPETIEDFWQ 60
 Db 188 QNRDKNRYDILPYDSTRVPLGKNDKYNINASYIRIVNHEEYFYIATQGLPETIEDFWQ 247
 QY 61 MVLNNCNVIMTRIEGCVIKCYWPIISKLEPEFEHFSVLETFHTVQVTVRVFQ 120
 Db 248 MVLNNCNVIMTRIEGCVIKCYWPIISKLEPEFEHFSVLETFHTVQVTVRVFQ 307
 QY 121 IVKSTGKSCQVKHLQFTKWPDPHTPASADFFIKYRVYRKSHITGPLLHCSAGVGRG 180
 Db 308 IVKSTGKSCQVKHLQFTKWPDPHTPASADFFIKYRVYRKSHITGPLLHCSAGVGRG 367
 QY 181 VFCVDWFSALEKNYSFDMINIVTQMRQRCGMIOTK 218
 Db 368 VFCVDWFSALEKNYSFDMINIVTQMRQRCGMIOTK 405
 RESULT 4
 ID AAE37994
 XX AAE37994 standard; protein; 261 AA.
 AC AAE37994;
 XX
 DT 06-NOV-2003 (first entry)
 XX Human kinase and phosphatase (KPP-39) protein.
 DE
 DE Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis;
 KW atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer;
 KW thrombocytopenia; developmental disorder; Reiter's syndrome;
 KW renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease;
 KW neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis;

KW autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome;
 KW acquired immune deficiency syndrome; immunosuppressive; Crohn's disease;
 KW neutropenic; dermatitis; multiple sclerosis; diabetes mellitus;
 KW allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome;
 KW osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological;
 KW gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.
 XX Homo sapiens.
 OS
 XX WO2003050084-A2.
 PN
 XX 19-JUN-2003.
 PD
 XX 06-DEC-2002; 2002WO-US039126.
 PF
 XX 07-DEC-2001; 2001US-0340235P.
 PR 19-DEC-2001; 2001US-0343007P.
 PR 21-DEC-2001; 2001US-0343546P.
 PR 04-FEB-2002; 2002US-0354388P.
 PR 15-FEB-2002; 2002US-0357675P.
 XX (INCY-) INCYTE GENOMICS INC.
 PA
 XX Kable AE, Chien D, Wilson AD, Swarnakar A, Gorvad AE;
 PI Hafalia AJA, Emerling BM, Ramkumar J, Jin P, Griffin JA, Marquis JP;
 PI Baughn MR, Chawla NK, Lehr-Mason PM, Khare R, Lee S, Hawkins PR;
 PI Becha SD, Lee SY, Sprague WW, Zabarjadian Y;
 XX WPI; 2003-532894/50.
 DR N-PSDB; AAD57366.
 DR
 XX New human kinases and phosphatases and polynucleotides, useful for
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
 PT cancer or hepatitis.
 XX
 PS Claim 1; Page 242; 282pp; English.
 XX The invention relates to an isolated polypeptide, which is a human kinase
 CC and phosphatase (KPP). KPP agonists and antagonists are useful for
 CC diagnosing, treating or preventing disorders associated with aberrant
 CC expression of KPP, particularly cell proliferative disorders (e.g.
 CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal
 CC nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary
 CC thrombocytopenia or cancer), developmental disorders (eg. renal tubular
 CC acidosis, anaemia or mental retardation), neurological disorders (e.g.
 CC Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/
 CC inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome,
 CC allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's
 CC disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,
 CC gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome,
 CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
 CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
 CC bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP
 CC is useful in assessing the effects of exogenous compounds on the
 CC expression of nucleic acids and kinases and phosphatases. KPP gene is
 CC useful in gene therapy and for creating transgenic animals to model human
 CC disease. The present sequence is human KPP protein
 XX
 SQ Sequence 261 AA;
 Query Match 80.0%; Score 1003; DB 6; Length 261;
 Best Local Similarity 78.9%; Pred. No. 3.5e-107;
 Matches 183; Conservative 24; Mismatches 25; Indels 0; Gaps 0;
 QY 2 NEDKNRYDILPYDSTRVPLGKNDKYNINASYIRIVNHEEYFYIATQGLPETIEDFWQ 61
 Db 24 NREKNRYDILPYDSTRVPLGKNDKYNINASYIRIVNHEEYFYIATQGLPETIEDFWQ 83
 QY 62 VLENNCNVIMTRIEGCVIKCYWPIISKLEPEFEHFSVLETFHTVQVTVRVFQ 121
 Db 84 VLENNCNVIMTRIEGCVIKCYWPIISKLEPEFEHFSVLETFHTVQVTVRVFQ 143

QY 122 VKSTGKSCQVHLOFTKWPDHGTSPASADFFIKYVYVVKSHITGTLVHCSAGVGTGV 181
Db 144 VEKSTGTSVSKQLQFTKWPDHGTSPASADSFYKYRYARKSHLTGPMVHCSAGIGRTGV 203
QY 182 FICVDVVFSAIEKNYSFDIMNVTQMRKCGMIQTKEQYQFCYEIVLEVLQ 233
Db 204 FLCVDVVFCAIVKNCNCFNMDIVAQMREQRSGMVQTKQYHCYDVLVLEVL 255
RESULT 5
AAE14454
ID AAE14454 standard; protein; 420 AA.
XX AAE14454;
XX 26-MAR-2002 (first entry)
XX Human protein phosphatase-4.
XX Human; protein phosphatase; PP-4; immune system disorder; AIDS; allergy;
KW neurological disorder; developmental disorder; Alzheimer's disease;
KW cell proliferative disorder; Huntington's disease; arteriosclerosis;
KW renal tubular acidosis; gonadal dysgenesis; cancer; adenocarcinoma;
KW leukemia; transgenic animal; gene therapy.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Region 183..411
FT /note= "Protein-tyrosine phosphatase"
FT Active-site 340..388
FT /note= "Tyrosine specific protein phosphatase active
FT site"
FT Region 351..363
FT /note= "Tyr_phosphatase"
FT Domain 362..379
FT /label= Transmembrane_domain
XX WO200196546-A2.
XX
XX 20-DEC-2001.
XX
XX 14-JUN-2001; 2001WO-US019442.
XX
XX 16-JUN-2000; 2000US-0212447P.
XX 22-JUN-2000; 2000US-0213746P.
XX 29-JUN-2000; 2000US-0215210P.
XX 06-JUL-2000; 2000US-0216529P.
XX 12-JUL-2000; 2000US-0218080P.
XX 21-JUL-2000; 2000US-0220117P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Au-Young J, Baughn MR, Ding L, Elliott VS, Gandhi AR, Griffin JA;
PI Hafalia A, Kearney L, Lee EA, Lu Y, Nguyen DB, Patterson C;
PI Rankumar J, Reddy R, Sanjanwala MS, Stewart EA, Tang YT, Thornton M;
PI Tribouley CM, Wallia NK, Yang J, Yao MG, Yue H;
XX
XX WPI; 2002-090206/12.
XX N-PSDB; AAD24022.
XX
XX Novel polypeptide, useful for diagnosing, treating or preventing
XX disorders of growth and development, immune system, neurological and cell
XX proliferation diseases, comprises cancer protein phosphatase
XX polypeptides.
XX
XX Claim 1; Page 105-106; 116pp; English.
XX
XX The present sequence is human protein phosphatase (PP)-4. PP
XX polynucleotide and polypeptide are useful in the diagnosis, treatment and
XX prevention of immune system disorders, neurological disorders,
XX developmental disorders and cell proliferative disorders. Examples of
XX immune system disorders include acquired immune deficiency syndrome

(AIDS), severe combined immunodeficiency disease (SCID), adult
respiratory distress syndrome, allergies, amyloidosis, anaemia, asthma,
atherosclerosis, Crohn's disease, atopic dermatitis, diabetes mellitus,
emphysema, Goodpasture's syndrome, gout, Graves' disease, multiple
sclerosis, myasthenia gravis, myocardial or pericardial inflammation,
osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
rheumatoid arthritis, Sjogren's syndrome, scleroderma, systemic
sclerosis, trauma; neurological disorders include Alzheimer's disease,
Huntington's disease, dementia, epilepsy, Parkinson's disease, mental
retardation and other developmental disorders of central nervous system
such as Down's syndrome, cerebral palsy, periodic paralysis, seasonal
disorders including mood, anxiety, and schizophrenia disorders, seasonal
affective disorder such as akathisia, amnesia, catatonia, dyskinesia;
developmental disorders include e.g. renal tubular acidosis, Duchenne and
Becker muscular dystrophy, gonadal dysgenesis, hypothyroidism; cell
proliferative disorders include e.g. actinic keratosis, arteriosclerosis,
atherosclerosis, bursitis, cirrhosis, hepatitis, psoriasis and cancer
including adenocarcinoma, leukaemia. The polypeptide and polynucleotide
are further useful for analysing proteome of a tissue or a cell type, for
screening an agonist/antagonist, a compound that specifically binds to it
or its modulator. The polynucleotide is useful for creating knockin
humanised animals (pigs) or transgenic animals (mice or rats) to model
human disease, for generating a transcript image of a tissue or cell
type, which represents the global pattern of gene expression by a
particular tissue or cell type
XX
SQ Sequence 420 AA;
Query Match 80.0%; Score 1003; DB 5; Length 420;
Best Local Similarity 78.9%; Pred. No. 7e-107;
Matches 183; Conservative 24; Mismatches 25; Indels 0; Gaps 0;
QY 2 NRDKNYRDLPYDSTRVPLGKKNKYNINASYIRVNHHEEYFYIATQGPETIEPQW 61
Db 183 NRKNRYRDLPYDSTRVPLGKSKDYNINASYIRVNCGEYFYIATQGPLLSTIDPQW 242
QY 62 VLENNCNVIAMITREIECGVVKISYWPISLKPFEHFSVLEFHVYQYTVRVFOI 121
Db 243 VLENNSNVIAMITREIEGGIKCYHYWPIISLKKPLELKHFRVFLNNYQILQYFIIRMFQV 302
QY 122 VKYSTGKSCQVHLOFTKWPDHGTSPASADFFIKYVYVVKSHITGTLVHCSAGVGTGV 181
Db 303 VEKSTGTSVSKQLQFTKWPDHGTSPASADSFYKYRYARKSHLTGPMVHCSAGIGRTGV 362
QY 182 FICVDVVFSAIEKNYSFDIMNVTQMRKCGMIQTKEQYQFCYEIVLEVLQ 233
Db 363 FLCVDVVFCAIVKNCNCFNMDIVAQMREQRSGMVQTKQYHCYDVLVLEVL 414
RESULT 6
ABG30845
ID ABG30845 standard; protein; 398 AA.
XX AC ABG30845;
XX 21-OCT-2002 (first entry)
XX Human tyrosine phosphatase protein #1.
XX
XX Human; tyrosine phosphatase; obesity; diabetes; Parkinson's disease;
KW central nervous system disorder; CNS; cardiovascular disorder; stroke;
KW chronic obstructive pulmonary disease; cancer; multiple sclerosis;
KW Alzheimer's disease; Huntington's disease; congestive heart failure;
KW myocardial infarction; chromosome 10.
XX
XX Homo sapiens.
XX WO200242435-A2.
XX 30-MAY-2002.
XX 27-NOV-2001; 2001WO-EP01379A.
XX

27-NOV-2000; 2000US-0252912P.
(FARB) BAYER AG.
Zhu Z;
WPI; 2002-575236/61.
N-PSDB; ABK9178.
New human tyrosine phosphatase polypeptide, the regulation of which is useful for treating obesity, diabetes, cardiovascular or central nervous system disorder, chronic obstructive pulmonary disease and cancer.
Claim 25; Fig 2; 145pp; English.
The present invention relates to a new human tyrosine phosphatase polypeptide. The invention is useful for the preparation of a medicament for modulating the activity of human tyrosine phosphatase in a disease such as obesity, diabetes, a central nervous system (CNS) disorder, chronic obstructive pulmonary disease, cardiovascular disorder or cancer. The invention is useful for treating a human tyrosine phosphatase dysfunction related disease, preferably the above mentioned diseases. The invention is useful for treating the above mentioned disorders, where the CNS disorder is selected from Parkinson's disease, multiple sclerosis, stroke, Alzheimer's disease, and Huntington's disease, and the cardiovascular disorder is selected from congestive heart failure and myocardial infarction. The molecules of the invention are useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to disease and abnormalities related to the presence of mutations in the polynucleotide coding the polypeptide of the invention. The present amino acid sequence represents the human tyrosine phosphatase protein #1 of the invention. This sequence is encoded by the human tyrosine phosphatase gene located on chromosome 10
Sequence 398 AA;
Query Match 79.4%; Score 995; DB 5; Length 398;
Best Local Similarity 78.0%; Pred. No. 5.5e-106;
Matches 181; Conservative 26; Mismatches 25; Indels 0; Gaps 0;
QY 2 NRDKNRYRDLVDSRVLGKNDYINASYRIVNHEEYFYIATQGLPFIETDFWQM 61
Db 161 NREKNRYRDLVDSRVLGKNDYINASYRIVNHEEYFYIATQGLPFIETDFWQM 220
QY 62 VLENNCNVAMITREICGVTKCYWPISLKPELEFHSVFLETHVTQYFTRVFQI 121
Db 221 VLENNCNVAMITREMEGGIICVHYWPISLKPELEFHSVFLETHVTQYFTRVFQI 280
QY 122 VKKSTGSKQCVKHLQFTKWDHGTTPASADFFIKYRVYRKSHITGPILVHCSAGVGTGV 181
Db 281 VEKSTGSHSVKQLQFTKWDHGTTPASADSFYKIRYARKSHITGPILVHCSAGVGTGV 340
QY 182 FICVDVWVFAIEKNYSFDIMNIVTQMRKQRCGMIOKEQYFCYEVILEVLQ 233
Db 341 FLCVDVWVFAIVKDCSFNIMDIVAQMRQSGSWQTKQYHFCYDILEVLQ 392
RESULT 7
ADD89795
ID ADD89795 standard; protein; 398 AA.
AC ADD89795;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human DKFZP566K0524 protein SEQ ID NO:10.
XX
KW cancer associated phosphatase; enzyme; human; cancer; tumour; cytostatic; immunosuppressive; antidiabetic; neuroprotective; antirheumatic; antiarthritic; antipsoriatic; antiarteriosclerotic; antiinflammatory; vulnary; gynaecological; antiangiogenic; hyperproliferative disease; autoimmune disease; diabetes mellitus; multiple sclerosis; rheumatoid arthritis; psoriasis; atherosclerosis; inflammation; scarring;
KW

Db 341 FLCVDVWFCAIVKDCSFNIMDIVAQMRQSRGSMVQTKQYHFCYDVLVLR 392

RESULT 8

ADE09123

ID ADE09123 standard; protein; 409 AA.

AC ADE09123;

XX

XX 29-JAN-2004 (first entry)

DT

XX

XX Novel protein-related contig polypeptide sequence #189.

DE

XX novel gene; novel protein; tissue marker; molecular weight marker;

KW chromosome marker; genetic disorder; contig.

KW

XX Unidentified.

OS

XX WO2003054152-A2.

XX

XX 03-JUL-2003.

XX

XX 10-DEC-2002; 2002WO-US039555.

XX

XX 10-DEC-2001; 2001US-0339739P.

PR

XX 11-DEC-2001; 2001US-0339453P.

PR

XX 14-MAR-2002; 2002US-0365091P.

PR

XX 14-MAR-2002; 2002US-0365384P.

PR

XX 14-MAR-2002; 2002US-0372381P.

PR

XX 12-APR-2002; 2002US-0372615P.

PR

XX 22-APR-2002; 2002US-00128558.

PR

XX 24-APR-2002; 2002US-0376045P.

XX

XX (HYSE-) HYSEQ INC.

PA

XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;

PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;

PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;

PI

XX WPI; 2003-569235/53.

XX

XX New polynucleotides, useful for expressing recombinant proteins for

PT analysis, characterization or therapeutic use, or as markers for tissues

PT in which the corresponding protein is preferentially expressed.

PT

XX Disclosure; SEQ ID NO 2667; 1177pp; English.

PS

XX The invention comprises the amino acid and coding sequences of novel

CC proteins. The DNA and protein sequences of the invention are useful as:

CC markers for tissues in which the corresponding protein is preferentially

CC expressed; as molecular weight markers on gels; as chromosome markers or

CC tags; to identify chromosomes or to map related gene positions; and to

CC compare with endogenous DNA sequences in patients to identify potential

CC genetic disorders. The present amino acid sequence was used in the

CC exemplification of the invention.

CC

XX SQ Sequence 409 AA;

XX

Query Match 79.4%; Score 995; DB 7; Length 409;

Best Local Similarity 78.0%; Pred. No. 5.7e-106;

Matches 181; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

QY 2 NRDKNRYRDLDPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPTIEDFWQM 61

Db 172 NREKNRYRDLDPYDSTRVPLGSKDYINASYIRIVNCGEYFYIATQGPLLSTIDDFWQM 231

QY 62 VLENNCNVIMTITREIECGVIKCYSWPISLKEPFEHFSVLEFTHVTFYVVRVFOI 121

Db 232 VLENNSNVIMITREMEGGIICKYHWYWPISLKKPLEKHFVLENYQILQYFIIRMFQV 291

QY 122 VKKSTGSCVCKHLOFTKWDHGTCPASADFFIKYRVYVRKSHITGLPLVHCAGVGRGV 181

Db 292 VEKSTGTSVSKVQLQFTKVPDHDGTCPASADSFIKYIRYAKSHLTGPMVHCAGIGRTGV 351

QY 182 FICVDVWFSAIEKNYSFDIMNIVTQMRKQRCMIOTKEQYQFCYHIVLEVLQ 233

Db 352 FLCVDVWFCAIVKDCSFNIMDIVAQMRQSRGSMVQTKQYHFCYDVLVLR 403

RESULT 9

ADE08106

ID ADE08106 standard; protein; 508 AA.

XX

XX ADE08106;

XX

XX 29-JAN-2004 (first entry)

DT

XX

XX Novel protein (useful for identifying genetic disorders) #261.

DE

XX novel gene; novel protein; tissue marker; molecular weight marker;

KW chromosome marker; genetic disorder.

KW

XX Unidentified.

OS

XX WO2003054152-A2.

XX

XX 03-JUL-2003.

XX

XX 10-DEC-2002; 2002WO-US039555.

XX

XX 10-DEC-2001; 2001US-0339739P.

PR

XX 11-DEC-2001; 2001US-0339453P.

PR

XX 14-MAR-2002; 2002US-0365091P.

PR

XX 14-MAR-2002; 2002US-0365384P.

PR

XX 12-APR-2002; 2002US-0372381P.

PR

XX 12-APR-2002; 2002US-0372615P.

PR

XX 22-APR-2002; 2002US-00128558.

PR

XX 24-APR-2002; 2002US-0376045P.

XX

XX (HYSE-) HYSEQ INC.

PA

XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;

PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;

PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;

PI

XX WPI; 2003-569235/53.

XX

XX N-PSDB; ADE07195.

XX

XX New polynucleotides, useful for expressing recombinant proteins for

PT analysis, characterization or therapeutic use, or as markers for tissues

PT in which the corresponding protein is preferentially expressed.

PT

XX Claim 20; SEQ ID NO 1172; 1177pp; English.

XX

XX The invention comprises the amino acid and coding sequences of novel

CC proteins. The DNA and protein sequences of the invention are useful as:

CC markers for tissues in which the corresponding protein is preferentially

CC expressed; as molecular weight markers on gels; as chromosome markers or

CC tags; to identify chromosomes or to map related gene positions; and to

CC compare with endogenous DNA sequences in patients to identify potential

CC genetic disorders. The present amino acid sequence represents a protein

CC of the invention.

CC

XX SQ Sequence 508 AA;

XX

Query Match 79.4%; Score 995; DB 7; Length 508;

Best Local Similarity 78.0%; Pred. No. 7.8e-106;

Matches 181; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

QY 2 NRDKNRYRDLDPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPTIEDFWQM 61

Db 271 NREKNRYRDLDPYDSTRVPLGSKDYINASYIRIVNCGEYFYIATQGPLLSTIDDFWQM 330

QY 62 VLENNCNVIMTITREIECGVIKCYSWPISLKEPFEHFSVLEFTHVTFYVVRVFOI 121

Db 331 VLENNSNVIMITREMEGGIICKYHWYWPISLKKPLEKHFVLENYQILQYFIIRMFQV 390

QY 122 VKKSTGKSCVKHLQFTKWDHGTGPASADFFIKYRVYRKSHITGPLLHCSAGVGTGV 181
Db 391 VEKSTGTSVSKQLQFTKWDHGTGPASADFFIKYRVYRKSHITGPLLHCSAGVGTGV 450
QY 182 FICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOQKEQYQFCVEIVLEVLQ 233
Db 451 FLCVDVVFAIVKDCSFNIMDIVAQMREQRSGMVQTKQHFCDIVLEVLIR 502

RESULT 10
ABG06042
ID ABG06042 standard; protein; 561 AA.
XX AC ABG06042;
XX 13-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #6033.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Dmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
XX DR N-PSDB; AAS70229.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX PS Claim 20; SEQ ID NO 36401; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 561 AA;

Query Match

79.4%; Score 995; DB 4; Length 561;

Best Local Similarity 78.0%; Pred. No. 9e-106;
Matches 181; Conservative 26; Mismatches 25; Indels 0; Gaps 0;
QY 2 NRDKNRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETEDFWQM 61
Db 324 NREKNRYRDLIPYDSTRVPLGKSKDYINASYIRIVNCGEYFYIATQGPLLSITDDFWQM 383
QY 62 VLENNCNVIAMITREIECGVIKCYSWPTSLKBPLEFEPHFVSFLETHVTHYQYFTRVFOI 121
Db 384 VLENNCNVIAMITREMEGGIICKYHYWPIISKKPLELKHFRVPLENYQILQYFTIRMFQV 443
QY 122 VKKSTGKSCVKHLQFTKWDHGTGPASADFFIKYRVYRKSHITGPLLHCSAGVGTGV 181
Db 444 VEKSTGTSVSKQLQFTKWDHGTGPASADFFIKYRVYRKSHITGPLLHCSAGVGTGV 503
QY 182 FICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOQKEQYQFCVEIVLEVLQ 233
Db 504 FLCVDVVFAIVKDCSFNIMDIVAQMREQRSGMVQTKQHFCDIVLEVLIR 555

RESULT 11

AAE37996
ID AAE37996 standard; protein; 412 AA.
XX AC AAE37996;
XX DT 06-NOV-2003 (first entry)
XX DE Human kinase and phosphatase (KPP-41) protein.
XX KW Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis;
KW atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer;
KW psoriasis; thrombocytopenia; developmental disorder; Reiter's syndrome;
KW renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease;
KW neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis;
KW autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome;
KW acquired immune deficiency syndrome; immunosuppressive; Crohn's disease;
KW neutropenic; dermatitis; multiple sclerosis; diabetes mellitus;
KW allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome;
KW osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological;
KW gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.
XX OS Homo sapiens.
XX PN WO2003050084-A2.
XX PD 19-JUN-2003.
XX PF 06-DEC-2002; 2002WO-US039126.
XX PR 07-DEC-2001; 2001US-0340235P.
XX PR 19-DEC-2001; 2001US-0343007P.
XX PR 21-DEC-2001; 2001US-0343546P.
XX PR 04-FEB-2002; 2002US-0354388P.
XX PR 15-FEB-2002; 2002US-0357675P.
XX (INCY-) INCYTE GENOMICS INC.
XX PA Kable AE, Chien D, Wilson AD, Swarnakar A, Gorvad AE;
XX PI Hafalia AJA, Emerling BM, Rankumar J, Jin P, Griffin JA, Marquis JP;
XX PI Baughn WR, Chawla NK, Lehr-Mason PM, Khare R, Lee S, Hawkins PR;
XX PI Becha SD, Lee SY, Sprague WW, Zebarjadian Y;
XX WIPI; 2003-532894/50.
XX N-PSDB; AAD57368.
XX DR New human kinases and phosphatases and polynucleotides, useful for
XX diagnosing, treating or preventing autoimmune or inflammatory disorders
XX (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
XX cancer or hepatitis.
XX PS Claim 1; Page 243-244; 282pp; English.

CC The invention relates to an isolated polypeptide, which is a human kinase
CC and phosphatase (KPP). KPP agonists and antagonists are useful for
CC diagnosing, treating or preventing disorders associated with aberrant
CC expression of KPP, particularly cell proliferative disorders (e.g.
CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal
CC nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary
CC thrombocytopaenia or cancer), developmental disorders (eg. renal tubular
CC acidosis, anaemia or mental retardation), neurological disorders (e.g.
CC Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/
CC inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome,
CC allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's
CC disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,
CC gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome,
CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
CC bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP
CC is useful in assessing the effects of exogenous compounds on the
CC expression of nucleic acids and kinases and phosphatases. KPP gene is
CC useful in gene therapy and for creating transgenic animals to model human
CC disease. The present sequence is human KPP protein
XX
SQ Sequence 412 AA;

Query Match 75.1%; Score 941; DB 6; Length 412;
Best Local Similarity 78.9%; Pred. No. 1e-99;
Matches 172; Conservative 22; Mismatches 24; Indels 0; Gaps 0;
QY 2 NRDKNRYDILPYDSTRVPLGKNDYINASYIRVNHHEEYFYIATQGPLTIEDFWQM 61
Db 183 NREKNRYDILPYDSTRVPLGSKDYINASYIRVNGEYFYIATQGPLLSTIDDFWQM 242
QY 62 VLENNCNVMIATREIEGVIKCYWPIISLKEPLEHEHSVFLETHVQYFVVRVQI 121
Db 243 VLENNCNVMIATREIEGGIIKCYHYWPIISLKEPLEHGFVLENYQILOYFIIRFQV 302
QY 122 VKKSTGSKQCVKHLQFTKWPDPHGPASADFFIKVYRVKSHITGPLLHVSAGVGRGV 181
Db 303 VEKSTGSHSVKQVQFTKWPDPHGPASADFSIKVIRYARKSHLTGPMVHVSAGIGRTG 362
QY 182 FICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMITQKE 219
Db 363 FLCVDVVFCAIVKNCSEINMIVAQMRQSGMWQTK 400

RESULT 12
ADK71863
ID ADK71863 standard; protein; 348 AA.
XX ADK71863;
XX 20-MAY-2004 (first entry)
XX Human kinase and phosphatase KPP-40 protein.
DE human; kinase, phosphatase; KPP; cardiovascular; antiarteriosclerotic;
KW hypotensive; vasotropic; antiinflammatory; antiangiinal; anti-HIV;
KW antiallergic; antiaesthetic; immunosuppressive; antithyroid;
KW dermatologic; antidiabetic; nephrotropic; angiot; gastrointestinal;
KW neuroprotective; osteopathic; antiarthritic; neuropathic; ophthalmologic;
KW antiparasitic; antiparkinsonian; nootropic; anticonvulsant; hepatotropic;
KW antipneumatic; haemostatic; cytostatic; antilipaeamic; antiparasitic;
KW antihelminthic; antibacterial; virucide; procoagulant; fungicide;
KW cardiovascular disease; immune system; neurological; growth; development;
KW cell proliferation; viral; bacterial; fungal; parasitic; protozoan;
KW helminthic infection; transgenic; gene therapy; enzyme.

OS Homo sapiens.
XX
XX WO2004018641-A2.
XX
XX 04-MAR-2004.
XX
XX 25-AUG-2003; 2003WO-US026635.
PF

XX 26-AUG-2002; 2002US-0406172P.
PR 25-SEP-2002; 2002US-04131910P.
PR 27-SEP-2002; 2002US-0414296P.
PR 11-OCT-2002; 2002US-0417821P.
XX (INCY-) INCYTE CORP.
PA Baughn MR, Richardson TW, Marquis JP, Swarnakar A, Tang YT;
PI Becha SD, Emerling BM, Jin P, Wilson AD, Yue H, Gietzen KJ;
PI Chang H, Yang YG, Lee SY, Khare R, Elliott VS, Hafalia AJA;
PI Chawla NK, Ramkumar J, Gururajan R, Tribouley CM, Chien D, Tran UK;
PI Murage J;
XX WPI; 2004-226830/21.
DR N-PSDB; ADK71922.
XX New human kinases and phosphatases, useful for diagnosing, treating or
XX preventing atherosclerosis, hypertension, AIDS, allergy, multiple
XX sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
XX or hepatitis.
PS Claim 1; SEQ ID NO 40; 347pp; English.
XX The invention relates to a novel isolated polypeptide which is a human
XX kinase and phosphatase (KPP). The polypeptide of the invention
XX demonstrates cardiovascular, antiarteriosclerotic, hypotensive,
XX vasotropic, antiinflammatory, antiangiinal, anti-HIV, antiallergic,
XX antiaesthetic, immunosuppressive, antithyroid, dermatological,
XX antidiabetic, nephrotropic, angiot, gastrointestinal, neuroprotective,
XX osteopathic, antiarthritic, uropathic, ophthalmologic, antihelminthic,
XX antiparkinsonian, nootropic, anticonvulsant, hepatotropic, antipneumatic,
XX haemostatic, cytostatic, antilipaeamic, antiparasitic, antihelminthic,
XX antibacterial, virucide, procoagulant and fungicide activities. The
XX kinase and phosphatase (KPP) polynucleotides, polypeptides, agonists and
XX antagonists may be useful for diagnosing, treating or preventing
XX disorders such as cardiovascular diseases, immune system disorders,
XX neurological disorders, disorders affecting growth and development, cell
XX proliferative disorders and viral, bacterial, fungal, parasitic,
XX protozoan or helminthic infections. Furthermore, the molecules of the
XX invention may be useful for creating transgenic animals to model human
XX disease and during gene therapy. The current sequence is that of a human
XX KPP protein of the invention.

Sequence 348 AA;
Query Match 51.0%; Score 639; DB 8; Length 348;
Best Local Similarity 54.3%; Pred. No. 7.9e-65;
Matches 126; Conservative 18; Mismatches 16; Indels 72; Gaps 1;
QY 2 NRDKNRYDILPYDSTRVPLGKNDYINASYIRVNHHEEYFYIATQGPLTIEDFWQM 61
Db 183 NREKNRYDILPYDSTRVPLGSKDYINASYIRVNGEYFYIATQGPLLSTIDDFWQM 242
QY 62 VLENNCNVMIATREIEGVIKCYWPIISLKEPLEHEHSVFLETHVQYFVVRVQI 121
Db 243 VLENNCNVMIATREIEGGIIKCYHYWPIISLKEPLEHGFVLENYQILOYFIIRFQV 302
QY 122 VKKSTGSKQCVKHLQFTKWPDPHGPASADFFIKVYRVKSHITGPLLHVSAGVGRGV 181
Db 303 VEK-----
QY 182 FICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMITQKEQYFCYVILEVQ 233
Db 306 -----SFNIMIVAQMRQSGMWQTKQYHFCYDIVLEVL 342
RESULT 13
ABU70688
ID ABU70688 standard; protein; 766 AA.
XX
XX ABU70688;
AC

Wed Dec 1 14:18:27 2004

Db 1138 TLEDIQTREVRHSHLNFTAMPDHDHTPSQDDLLTFISYMRHHSRGPILTHCSAGIGRS 1197
QY 180 GVFIQVDVVFSAIEKNYSFDDIMNIVTQMRKQRCGMIQTKQYQFCYEVILEVL 232
Db 1198 GTLICIDVVLGLISQDLDFDISLVRMRLQRHGMVQTEQYIFCYQVILYVL 1250

RESULT 15
ID AAG67458 standard; protein; 1267 AA.
XX AC AAG67458;
XX DT 26-NOV-2001 (first entry)
XX DE Amino acid sequence of a human polypeptide.
XX KW Human; protein kinase; protein phosphatase; signal transduction;
KW intracellular signalling pathway.
XX OS Homo sapiens.
XX XN WO200109345-A1.
XX PD 08-FEB-2001.
XX PF 28-JUL-2000; 2000WO-JP005060.
XX PR 29-JUL-1999; 99JP-00248036.
PR 18-OCT-1999; 99US-0159590P.
PR 11-JAN-2000; 2000JP-00118776.
PR 17-FEB-2000; 2000US-0183322P.
PR 02-MAY-2000; 2000JP-00183767.
XX PA (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
PI Senoo C, Nezu J;
XX WPI; 2001-564736/63.
XX New genes encoding protein kinase and protein phosphatase, useful for
PT identifying modulators which can be used to treat human or animal
PT disorders associated with the expression or function of these enzymes.
XX Example 4; Page 305-315; 336pp; Japanese.

XX The specification describes human protein kinase/protein phosphatases.
CC The polypeptides are expected to participate in signal transduction in
CC cells. The kinase phosphatases are connected with intracellular
CC signalling pathways. Antisense oligonucleotides and compounds identified
CC by screening (agonists or antagonists) can be used to treat human or
CC animal disorders associated with the expression or function of the
CC protein. In addition, the polypeptides may be used as target molecules
CC for drug development. The present sequence represents a polypeptide, used
CC in the course of the invention

SQ Sequence 1267 AA;
Query Match 47.3%; Score 592.5; DB 4; Length 1267;
Best Local Similarity 47.6%; Pred. No. 1.2e-58; Indels 1; Gaps 1;
Matches 111; Conservative 41; Mismatches 80;
QY 1 QNRDNRYRDIILPYDSTRVPLGKNDKYNASVIRIVNHEEYFYIATQGLPETIEDFWQ 60
Db 1018 ENRRKNRYKNILPYDAIRVPLGDEGGINASRIKIPVGKEEFYIACQGLPTTVGDFWQ 1077
QY 61 MVLNENNCNVIAMITREICGVICYSWPISL-KEPLEFEHFSVFLETHVQYFTRVRF 119
Db 1078 MIWEQKSTVIAMWTQEVGEKIKQRYWPNILGKTTMVSNRULALVRMQQLKGFVVRAM 1137
QY 120 QIVKKSTGKSCQCVKHLQFTKWPDHGTPASADFFIKYRVYVRKSHITGPIIVHCSAGVGR 179

Db 1138 TLEDIQTREVRHSHLNFTAMPDHDHTPSQDDLLTFISYMRHHSRGPILTHCSAGIGRS 1197
QY 180 GVFIQVDVVFSAIEKNYSFDDIMNIVTQMRKQRCGMIQTKQYQFCYEVILEVL 232
Db 1198 GTLICIDVVLGLISQDLDFDISLVRMRLQRHGMVQTEQYIFCYQVILYVL 1250

Search completed: December 1, 2004, 12:11:57
Job time : 82.7544 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 1, 2004, 12:07:39 ; Search time 85.8421 Seconds
(without alignments)
1561.731 Million cell updates/sec

Title: US-09-095-478A-5_COPY_188_420

Perfect score: 1253

Sequence: 1 QNRDKRYRDLIPYDSTRP.....MIQKEQYQFCYIVLEVLQ 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1253	100.0	426	2	O55082 mus musculus
2	995	79.4	398	2	Q9Y406 homo sapien
3	607.5	48.5	2484	2	Q28006 bos taurus
4	598.5	47.8	2453	1	PTND_MOUSE
5	595.5	47.5	2500	2	Q6EH9 xenopus lae
6	592.5	47.3	2485	1	PTND_HUMAN
7	510	40.7	920	2	Q6GPK7 xenopus lae
8	500	39.9	292	2	Q8N4S3
9	499	39.8	913	1	PTN3_HUMAN
10	493.5	39.4	926	2	Q9WU22
11	488.5	39.0	1948	1	PTNS_HUMAN
12	486.5	38.8	2051	2	Q44328
13	485.5	38.7	468	2	Q91BA0
14	485.5	38.7	615	2	Q91A18
15	484.5	38.7	468	2	Q91BA2
16	483.5	38.6	1502	2	Q9UM81
17	482.5	38.5	749	2	Q8R169
18	482.5	38.5	857	2	Q90YJ4
19	482.5	38.5	1254	2	Q8VBV0
20	480.5	38.3	468	2	Q9NL06
21	480.5	38.3	1222	2	Q8MY44
22	479.5	38.3	1100	2	Q8MY45
23	479.5	38.3	1187	2	Q8MY42
24	479.5	38.3	1202	2	Q8MY43
25	477.5	38.1	1896	2	Q91AJ1
26	476.5	38.0	926	1	PTN4_HUMAN
27	475.5	37.9	907	2	Q8MY41
28	475	37.9	1337	1	PTFU_HUMAN
29	474.5	37.9	1501	2	Q7TT17
30	474.5	37.9	1501	2	Q9QW00
31	474.5	37.9	1863	2	Q64605 rattus norv

32	474.5	37.9	1904	2	Q64699
33	474.5	37.9	1912	1	PTPD_HUMAN
34	473.5	37.8	469	2	Q9NL08
35	473.5	37.8	1998	2	Q8CIW2
36	472.5	37.7	929	2	Q6NRP9
37	472.5	37.7	929	2	Q6DCH9
38	472.5	37.7	929	2	AAH70687
39	471.5	37.6	469	2	Q9NLI1
40	471.5	37.6	1102	2	Q80VN7
41	471	37.6	1238	2	Q8K3Q2
42	471	37.6	1499	2	Q90815
43	470.5	37.5	579	2	Q9J307
44	470	37.5	634	2	Q6DE20
45	469.5	37.5	1956	2	Q6MZF6

Q64699 mus musculus
P23468 homo sapien
Q9nl08 eptatretus
Q8ciw2 mus musculus
Q9nrp9 xenopus lae
Q6dch9 xenopus lae
AAH70687 xenopus l
Q9nli1 brachiosto
Q80vn7 mus musculo
Q8k3q2 mus musculo
Q90815 gallus gall
Q9j307 mus musculo
Q6de20 xenopus lae
Q6mzf6 homo sapien

ALIGNMENTS

RESULT 1
O55082
ID O55082 PRELIMINARY; PRT; 426 AA.
AC O55082;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Protein-tyrosine-phosphatase (EC 3.1.3.48) (Mus musculus adult male
DE testis cDNA, RIKEN full-length enriched library, clone:4921505B14
DE product:protein tyrosine phosphatase, non-receptor type 20, full
DE insert sequence).
GN Name=Ptpn20;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=98070510; PubMed=9407093;
RA Ohsugi M., Kuramochi S., Matsuda S., Yamamoto T.;
RT "Molecular cloning and characterization of a novel cytoplasmic
RT protein-tyrosine phosphatase that is specifically expressed in
RT spermatocytes.";
RL J. Biol. Chem. 272:33092-33099 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX STRAIN=C57BL/6J; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=9279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes."

Genome Res. 10:1617-1630(2000).

[6]

SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Testis;

MEDLINE=20530913; PubMed=11076861;

Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,

Kono H., Akiyama J., Nishi K., Kitsumi T., Nishine T., Harada A.,

Sumi N., Ishii Y., Nakamura S., Ikegami T., Kashiwagi K.,

Yamamoto K., Matsumoto H., Sakaguchi S., Ohgami E., Watahiki M.,

Fujiwara S., Inoue K., Togawa Y., Izawa T., Matsura S., Kawai J.,

Okazaki Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-Format

sequencing pipeline with 384 multicapillary sequencer."

Genome Res. 10:1757-1771(2000).

[7]

SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Testis;

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,

Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

Tegawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

EMBL: D64141; BAA23761.1; -.

EMBL: AK029493; BAC26476.1; -.

HSSP: P10586; ILAR.

MGD; MGI:1196295; Ptpn20.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.

InterPro; IPR000387; TYR_PP.

InterPro; IPR000242; TYR_PP.

PFam; PF00102; Y_phosphatase; 1.

PRINTS; PR00700; PRTYPHPTASE.

SMART; SM00194; PTPC; 1.

PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.

PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.

PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.

Hydrolase; Receptor.

SEQUENCE 426 AA; 49118 MW; 2835FB13379502F4 CRC64;

Query Match 100.0%; Score 1253; DB 2; Length 426;

Best Local Similarity 100.0%; Pred. No. 1.4e-112;

Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNRDKNRYDILPYDSTRVPLGKNDYINASYIRVNHHEEYFYIATGQPLPETIEDFWQ 60

DB 188 QNRDKNRYDILPYDSTRVPLGKNDYINASYIRVNHHEEYFYIATGQPLPETIEDFWQ 247

QY 61 MVLNNCNVIAITREIECGVTKCYSPISLKEPFEHFSVLETFHTVQYFVVRVQ 120

DB 248 MVLNNCNVIAITREIECGVTKCYSPISLKEPFEHFSVLETFHTVQYFVVRVQ 307

QY 121 IVKSTGKSCQVKHLQFTKWDHGTTPASADFFIKVYVRKSHITGTPLLVHCSAGVGTG 180

DB 308 IVKSTGKSCQVKHLQFTKWDHGTTPASADFFIKVYVRKSHITGTPLLVHCSAGVGTG 367

QY 181 VFICVDVVFSAIEKNYSFIMNIVTQMRKQRCGMITQKEQYFCYFVLEVLQ 233

DB 368 VFICVDVVFSAIEKNYSFIMNIVTQMRKQRCGMITQKEQYFCYFVLEVLQ 420

RESULT 2

QY9406

QY9406 PRELIMINARY; PRT; 398 AA.

AC QY9406;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein DKFZP566K0524 (Fragment).

GN Name=DKFZP566K0524;

OS Homo sapiens (Human);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606;

RP [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RA Ansgorge W., Mirkner U., Mewes H.W., Gassenhuber J., Wiemann S.;

RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL050040; CAB43248.1; -.

DR PIR; T08716; T08716.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.

DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.

DR InterPro; IPR000387; TYR_PP.

DR InterPro; IPR000242; TYR_PP.

DR PFam; PF00102; Y_phosphatase; 1.

DR PRINTS; PR00700; PRTYPHPTASE.

DR SMART; SM00194; PTPC; 1.

DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.

DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.

DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.

KW Hydrolase; Hypothetical protein.

FT NON TER 1

FT SEQUENCE 398 AA; 45690 MW; 857AAD03747870A2 CRC64;

Query Match 79.4%; Score 995; DB 2; Length 398;

Best Local Similarity 78.0%; Pred. No. 1.2e-87;

Matches 181; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

QY 2 NRDKNRYDILPYDSTRVPLGKNDYINASYIRVNHHEEYFYIATGQPLPETIEDFWQ 61

DB 161 NRDKNRYDILPYDSTRVPLGKNDYINASYIRVNHHEEYFYIATGQPLPETIEDFWQ 220

QY 62 VLENNCNVIAITREIECGVTKCYSPISLKEPFEHFSVLETFHTVQYFVVRVQ 121

DB 221 VLENNCNVIAITREIECGVTKCYSPISLKEPFEHFSVLETFHTVQYFVVRVQ 280

QY 122 VKKSTGKSCQVKHLQFTKWDHGTTPASADFFIKVYVRKSHITGTPLLVHCSAGVGTG 181

DB 281 VKKSTGKSCQVKHLQFTKWDHGTTPASADFFIKVYVRKSHITGTPLLVHCSAGVGTG 340

QY 182 FICVDVVFSAIEKNYSFIMNIVTQMRKQRCGMITQKEQYFCYFVLEVLQ 233

DB 341 FLCVDVVFSAIEKNYSFIMNIVTQMRKQRCGMITQKEQYFCYFVLEVLQ 392

RESULT 3

QY9406 PRELIMINARY; PRT; 2484 AA.

AC QY9406;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-NOV-2004 (TrEMBLrel. 26, Last annotation update)

DE BAI4.

OS Bos taurus (Bovine);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovinae; Bos.

OC NCBI_TaxID=9913;

RP [1]

RP SEQUENCE FROM N.A.

RA Vega Q.C., Walton K.M., Dixon J.E.;

RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Contains 5 PDZ/DHR domains.

DB EMBL; U20807; AAA73516.1; -.

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DR HSSP; Q64512; 1GM1.
DR GO; GO:0005856; C:cytoskeleton; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR009065; FERM.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR011019; KIND.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR011036; PH related.
DR InterPro; IPR000387; Tyr phosphatase.
DR InterPro; IPR000242; Tyr_Pp.
DR Pfam; PF00373; Band_41; 1.
DR Pfam; PF00595; PDZ; 5.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00935; BAND41.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00295; B41; 1.
DR SMART; SM00750; KIND; 1.
DR SMART; SM00228; PDZ; 5.
DR SMART; SM00194; PTPc; 1.
DR PROSITE; PS00660; FERM_1; FALSE_NEG.
DR PROSITE; PS00661; FERM_2; FALSE_NEG.
DR PROSITE; PS00057; FERM_3; 1.
DR PROSITE; PS00106; PDZ_5.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
DR Hydrolase.
SQ SEQUENCE 2484 AA; 276382 MW; 45A92F0D4F1ED13D CRC64;

Query Match 48.5%; Score 607.5; DB 2; Length 2484;
Best Local Similarity 48.9%; Pred. No. 3.5e-49;
Matches 114; Conservative 40; Mismatches 78; Indels 1; Gaps 1;

QY 1 QNRDKNRYRDLIPDYSTRVPLGKNDYINASYIRVNHHEEYFIATOGPLPTIEDFWQ 60
Db :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2235 ENRKNRYNLLPYDTRVPLGDEGGYINASFIKIPVGREFFVYIACQGLPTTVGDFWQ 2294

QY 61 MVLNNCNVAMITREIECGVICKSYWPISL-KEPFEFEHFSVLETFHTVQYFVRVF 119
Db :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2295 MIWEQNSVIAAMTQVEGEKIKQRYWPNVLGKSTWNSRLALRVVQQLGFFVRAM 2354

QY 120 QIVKSKTGSKOCVKHLQFKWPHGTPASDFIKVYRVKSHITGPIILVHCSAGVGT 179
Db :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2355 TUEDIQTGEVRHVSHLNFATWPDHPTSPQPDLLTFISYMRHVHRSGPIITHCSAGIGRS 2414

QY 180 GVFIQVDVVFSALEKNYSFDIMNIVTQMRKRGCMQTKEOYFCYEVILEVL 232
Db :|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2415 GTLICIDVVLGLISQLEFDSLVRCMLQRHGMVQTEDQYIFCYQVILYL 2467

RESULT 4
PTND MOUSE
ID PTND MOUSE STANDARD; PRT; 2453 AA.
AC Q64512; Q61494; Q62135; Q64499;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 13 (EC 3.1.3.48)
DE (protein tyrosine phosphatase, PTP-BL) (protein-tyrosine phosphatase
DE RIP) (protein tyrosine phosphatase DP2PTP) (PTP36).
GN Name=Ptn13; Synonyms=Ptp14;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Skin;
RX MEDLINE=96340953; PubMed=8749712;
```

```
RA Hendriks W., Schepens J., Baechner D., Rijes J., Zeeuwen P.,
RA Zechner U., Hameister H., Wieringa B.;
RA "Molecular cloning of a mouse epithelial protein-tyrosine phosphatase
RT with similarities to submembranous proteins.";
RL J. Cell. Biochem. 59:418-430(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RC MEDLINE=95145716; PubMed=7843407;
RA Chida D., Kume T., Mukouyama Y., Tabata S., Nomura N., Thomas M.,
RA Watanabe T., Oishi M.;
RT "Characterization of a protein tyrosine phosphatase (RIP) expressed at
RT a very early stage of differentiation in both mouse erythroleukemia
RT and embryonal carcinoma cells.";
RL FEBS Lett. 358:233-239(1995).
RN [3]
RP SEQUENCE OF 1105-2452 FROM N.A.
RC STRAIN=CR 17 SCID; TISSUE=Thymus;
RX MEDLINE=94354845; PubMed=8074693;
RA Sawada M., Ogata M., Fujino Y., Hamaoka T.;
RT "cDNA cloning of a novel protein tyrosine phosphatase with homology to
RT cytoskeletal protein 4.1 and its expression in T-lineage cells.";
RL Biochem. Biophys. Res. Commun. 203:479-484(1994).
RN [4]
RP SEQUENCE OF 2267-2373 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=95134232; PubMed=7832766;
RA Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.;
RT "A novel receptor-type protein tyrosine phosphatase with a single
RT catalytic domain is specifically expressed in mouse brain.";
RL Biochem. J. 305:499-504(1995).
RN [5]
RP INTERACTION WITH PDLIM4.
RX MEDLINE=98155214; PubMed=9487134;
RA Cuppen E., Gerrits H., Peeters B., Wieringa B., Hendriks W.;
RT "PDZ motifs in PTP-BL and RIL bind to internal protein segments in the
RT LIM domain protein RIL.";
RL Mol. Biol. Cell 9:671-683(1998).
CC -!- FUNCTION: Regulates negatively FAS-induced apoptosis and NGFR-
CC mediated pro-apoptotic signaling.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBUNIT: Binds PLEKHA1 and PLEKHA2 through its first PDZ domain
CC (By similarity). Interacts with TRIP6 and TNFRSF6 (Fas receptor)
CC through its second PDZ domain. Interacts with the C-terminal SVP
CC motif of NGFR through its third PDZ domain. Interacts with the LIM
CC domain of PDLIM4 through its second and fourth PDZ domains.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed predominantly in kidney and, to a
CC lesser extent, in lung, heart, brain and testis.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -!- SIMILARITY: Contains 1 FERM domain.
CC -!- SIMILARITY: Contains 5 PDZ/DHR domains.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; Z32740; CAA83650.1; -
DR EMBL; D83966; BAA12158.1; -
DR EMBL; D28529; BAA05885.1; -
DR EMBL; Z23059; CAA80594.1; -
DR PIR; PT0601; PT0601.
DR PIR; PT0635; PT0696.
DR PIR; PT0649; PT0712.
DR PIR; S40290; S40290.
DR PIR; S71625; S71625.
DR PDB; 1GM1; NMR; A=1351-1444.
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DR	PDB: 1OZI; NMR: A=1351-1444.
DR	MGD; MGI:103293; Ptpn13..
DR	InterPro: IPR000299; Band_4.1.
DR	InterPro: IPR009065; FERM.
DR	InterPro: IPR001478; PDZ.
DR	InterPro: IPR000387; TYR phosphatase.
DR	InterPro: IPR000242; Tyr_PP.
DR	Pfam: PF00373; Band_41; 1.
DR	Pfam: PF00595; PDZ; 5.
DR	Pfam: PF00102; Y_phosphatase; 1.
DR	PRINTS: PR00935; BAND41.
DR	PRINTS: PR00700; PRTPHPTASE.
DR	SMART: SM00295; B41; 1.
DR	SMART: SM00228; PDZ; 5.
DR	SMART: SM00194; FPC; 1.
DR	SMART: SM00404; PTPC_motif; 1.
DR	PROSITE: PS00660; FERM_1; FALSE_NEG.
DR	PROSITE: PS00661; FERM_2; FALSE_NEG.
DR	PROSITE: PS0057; FERM_3; 1.
DR	PROSITE: PS0106; PDZ; 5.
DR	PROSITE: PS00383; TYR PHOSPHATASE_1; FALSE_NEG.
DR	PROSITE: PS0056; TYR_PHOSPHATASE_2; 1.
DR	PROSITE: PS0055; TYR_PHOSPHATASE_FTP; 1.
KW	3D-structure; Coiled coil; Cytoskeleton; Hydrolase;
KW	Protein phosphatase; Repeat; Coiled coil (Potential).
FT	DOMAIN 458 493
FT	DOMAIN 565 865
FT	DOMAIN 1084 1170
FT	DOMAIN 1357 1442
FT	DOMAIN 1491 1579
FT	DOMAIN 1764 1845
FT	DOMAIN 1857 1942
FT	DOMAIN 2180 2434
FT	ACT_SITE 2375 2375
FT	DOMAIN 56 59
FT	CONFLICT 79 81
FT	CONFLICT 156 168
FT	CONFLICT 233 233
FT	CONFLICT 306 306
FT	CONFLICT 322 322
FT	CONFLICT 381 381
FT	CONFLICT 822 822
FT	CONFLICT 1233 1233
FT	CONFLICT 1449 1449
FT	CONFLICT 1474 1489
FT	CONFLICT 1622 1622
FT	CONFLICT 1872 1872
FT	CONFLICT 1979 1979
FT	CONFLICT 2078 2078
FT	CONFLICT 2233 2233
FT	CONFLICT 2448 2452
FT	CONFLICT 2453 AA; 270332 MW; 53396P27AE2582F2 CRC64;
FT	CONFLICT 1622 1622
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FT	CONFLICT 1979 1979
FT	CONFLICT 2078 2078
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FT	CONFLICT 1622 1622
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FT	CONFLICT 1979 1979
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FT	CONFLICT 1979 1979
FT	CONFLICT 2078 2078
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FT	CONFLICT 1622 1622
FT	CONFLICT 1872 1872
FT	CONFLICT 1979 1979
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FT	CONFLICT 1872 1872
FT	CONFLICT 1979 1979
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FT	CONFLICT 1979 1979
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FT	CONFLICT 1622 1622
FT	CONFLICT 1872 1872
FT	CONFLICT 1979 1979
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FT	CONFLICT 2448 2452
FT	CONFLICT 2453 AA; 270332 MW; 53396P27AE2582F2 CRC64;
FT	CONFLICT 1622 1622
FT	CONFLICT 1872 1872
FT	CONFLICT 1979 1979
FT	CONFLICT 2078 2078
FT	CONFLICT 2233 2233
FT	CONFLICT 2448 2452
FT	CONFLICT 2453 AA; 270332 MW; 53396P27AE2582F2 CRC64;
FT	CONFLICT 1622 1622
FT	CONFLICT 1872 1872
FT	CONFLICT 1979 1979
FT	CONFLICT 2078 2078
FT	CONFLICT 2233 2233
FT	CONFLICT 2448 2452
FT	CONFLICT 2453 AA; 270332 MW; 53396P27AE2582F2 CRC64;
FT	CONFLICT 1622 1622
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FT	CONFLICT 1979 1979
FT	CONFLICT 2078 2078
FT	CONFLICT 2233 2233
FT	CONFLICT 2448 2452
FT	CONFLICT 2453 AA; 270332 MW; 53396P27AE2582F2 CRC64;
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FT	CONFLICT 1979 1979
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FT	CONFLICT 2453 AA; 270332 MW; 53396P27AE2582F2 CRC64;
FT	CONFLICT 1622 1622
FT	CONFLICT 1872 1872
FT	CONFLICT 1979 1979
FT	CONFLICT 2078 2078
FT	CONFLICT 2233 2233
FT	CONFLICT 2448 2452
FT	CONFLICT 2453 AA; 270332 MW; 53396P27AE2582F2 CRC64;
FT	CONFLICT 1622 1622

RN [2] SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Leukemia;
 RX MEDLINE=94116679; PubMed=8287977;
 RA Maekawa K., Imagawa N., Nagamatsu M., Harada S.;
 RT "Molecular cloning of a novel protein-tyrosine phosphatase containing
 RL a membrane-binding domain and GLGF repeats.";
 RL FEBS Lett. 337:200-206 (1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95014139; PubMed=7929060;
 RA Saras J., Claesson-Welsh L., Heldin C.-H., Gonez L.J.;
 RT "Cloning and characterization of PTP11, a protein tyrosine phosphatase
 RL with similarities to cytoskeletal-associated proteins.";
 RL J. Biol. Chem. 269:24082-24089 (1994).
 RN [4]
 RP SEQUENCE OF 1216-2490 FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=95232528; PubMed=7536343;
 RA Sato T., Irie S., Kitada S., Reed J.C.;
 RT "FAP-1: a protein tyrosine phosphatase that associates with Fas.";
 RL Science 268:411-415 (1995).
 RN [6]
 RP SEQUENCE OF 1323-1821 FROM N.A.
 RA Irie S., Hachiya T., Sato T.A.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 1323-1922 FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [8]
 RP INTERACTION WITH TRIP6.
 RX MEDLINE=99329089; PubMed=10400701;
 RA Murthy K.K., Clark K., Fortin Y., Shen S.-H., Barville D.;
 RT "ZRP-1, a zyxin-related protein, interacts with the second PDZ domain
 RL of the cytosolic protein tyrosine phosphatase hPTP1E.";
 RL J. Biol. Chem. 274:20679-20687 (1999).
 RN [9]
 RP INTERACTION WITH NGFR.
 RX MEDLINE=20012928; PubMed=10544233;
 RA Irie S., Hachiya T., Rabizadeh S., Maruyama W., Mukai J., Li Y.,
 RA Reed J.C., Bredesen D.E., Sato T.A.;
 RT "Functional interaction of Fas-associated phosphatase-1 (FAP-1) with
 RL p75(NTR) and their effect on NF-kappaB activation.";
 RL FEBS Lett. 460:191-198 (1999).
 RN [10]
 RP INTERACTION WITH PLEKHA1 AND PLEKHA2.
 RX PubMed=14516276; DOI=10.1042/BJ20031154;
 RA Kimber W.A., Deak M., Prescott A.R., Alessi D.R.;
 RT "Interaction of the protein tyrosine phosphatase PTP11 with the
 RL Ptdins(3,4)P2-binding adaptor protein TAPP1.";
 RL Biochem. J. 376:525-535 (2003).
 RN [11]
 RP STRUCTURE BY NMR OF 1361-1456 UNCOMPLEXED AND IN COMPLEX WITH THE
 RC C-TERMINUS OF TNFRSF6.
 RX MEDLINE=20170882; PubMed=10704206;
 RA Kozlov G., Gehring K., Ekiel I.;
 RT "Solution structure of the PDZ2 domain from human phosphatase hPTP1E
 RL and its interactions with C-terminal peptides from the Fas receptor.";
 RL Biochemistry 39:2572-2580 (2000).
 RN [12]
 RP STRUCTURE BY NMR OF 1361-1456 IN COMPLEX WITH THE C-TERMINUS OF THE
 RC GUANINE NUCLEOTIDE EXCHANGE FACTOR RA-GEF-2.
 RX MEDLINE=22090786; PubMed=12095257; DOI=10.1016/S0022-2836(02)00544-2;
 RA Kozlov G., Banville D., Gehring K., Ekiel I.;
 RT "Solution structure of the PDZ2 domain from cytosolic human
 RL phosphatase hPTP1E complexed with a peptide reveals contribution of
 RL the beta2-beta3 loop to PDZ domain-ligand interactions.";
 RL J. Mol. Biol. 320:813-820 (2002).
 RN [13]
 RP VARIANTS PRO-1419 AND MET-1522.
 RX MEDLINE=22333362; PubMed=12436199; DOI=10.1007/s100380200094;
 RA Yoshida S., Harada H., Nagai K., Fukino K., Teramoto A., Emi M.;
 RT "Head-to-head juxtaposition of Fas-associated phosphatase-1 (FAP-1)
 RL and c-Jun NH2-terminal kinase 3 (JNK3) genes: genomic structure and
 RL seven polymorphisms of the FAP-1 gene.";
 RL J. Hum. Genet. 47:614-619 (2002).
 CC -1- FUNCTION: Regulates negatively Fas-induced apoptosis and NGFR-
 CC mediated pro-apoptotic signaling.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBUNIT: Interacts with TRIP6 and TNFRSF6 (Fas receptor) through
 CC its second PDZ domain. Interacts with the C-terminal SVP motif of
 CC NGFR through its third PDZ domain. Interacts with the LIM domain
 CC of PDLIM4 through its second and fourth PDZ domains. Binds PLEKHA1
 CC and PLEKHA2 through its first PDZ domain.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1;
 CC IsoId=Q12923-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q12923-2; Sequence=VSP_000496;
 CC Name=3;
 CC IsoId=Q12923-3; Sequence=VSP_000497;
 CC Name=4;
 CC IsoId=Q12923-4; Sequence=VSP_007921;
 CC Note=May be due to a competing donor splice site;
 CC -1- TISSUE SPECIFICITY: Present in most tissues with the exception of
 CC the liver and skeletal muscle. Most abundant in lung, kidney and
 CC fetal brain.
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Non-receptor class subfamily.
 CC -1- SIMILARITY: Contains 1 FERM domain.
 CC -1- SIMILARITY: Contains 5 PDZ/DHR domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U12128; AAB60339.1; -
 DR EMBL; D21209; BAA04750.1; -
 DR EMBL; D21210; BAA04751.1; -
 DR EMBL; D21211; BAA04752.1; -
 DR EMBL; X80289; CAA56563.1; -
 DR EMBL; X79676; CAA56124.1; -

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DR EMBL; L34583; AAC41755.1; -.
DR EMBL; AF233323; RAF63474.1; -.
DR EMBL; BC039610; AAH39610.1; ALT_TERM.
DR PIR; A54971; A54971.
DR PIR; I67629; I67629.
DR PIR; I67630; I67630.
DR PDB; 1D5G; NMR; A=1361-1456.
DR PDB; 1Q7X; NMR; A=1357-1459.
DR PDB; 3PDZ; NMR; A=1361-1456.
DR Genew; HGNC:9646; PTPN13.
DR MIM; 60267; -.
DR GO; GO:004725; P:protein-tyrosine-phosphatase activity; TAS.
DR GO; GO:006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR009065; FERM.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR011036; PH-related.
DR InterPro; IPR000387; Tyr_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00373; Band 41; 1.
DR Pfam; PF00595; PDZ; 5.
DR PRINTS; PR00935; BAND41.
DR PRINTS; PR00700; PRTYPHPTASE.
DR PROSITE; PS00660; FERM_1; FALSE_NEG.
DR PROSITE; PS00661; FERM_2; FALSE_NEG.
DR PROSITE; PS00057; FERM_3; 1.
DR PROSITE; PS0106; PDZ; 5.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.

Query Match 47.3%; Score 592.5; DB 1; Length 2485;
Best Local Similarity 47.6%; Pred. No. le-47;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;

QY 1 QNRDKNRYDILPYDSTRVPLGKKNKYINASYIRIVNHEEYFYIATGQPLPETIEDFWQ 60
DB 2236 ENREKNRYKNILPYDATRVPLGDSGGYINASFILKIPVGEFVIACQPLPTTVGVDFWQ 2295
QY 61 MVLNNNCNVNIAMITREIECGVIKCYSPISL-KEPLEFEHFSVLETFHVTQYTFVVF 119
DB 2296 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTVSNRLRLALVRMQQLKGFVVRAM 2355
QY 120 QIVKSTGKSCVXHLQTKWPDHGTASADFFIKYVYVRKSHITGTLVHCAGVGT 179
DB 2356 TLEDIQTRVHRHISHLNFTAPDHDTPSQDDLTFTFSYMRHHRSGPIITHCAGIGRS 2415
QY 180 GVFCVDVVFSAIEKNYSFDMNIVTQMKRKGCMIQKEQYQFCYEIVLEVL 232
DB 2416 GTLICIDVVLGLISODLDFDISDLVRCLRHGMVQIEDQYIFCYQVILYVL 2468

RESULT 7
ID Q6GPK7 PRELIMINARY; PRT; 920 AA.
AC Q6GPK7;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Shevchenko Y., Bouffard G.G.,
Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Krzyszinski M.I., Marra M.A.;
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Oocytes;
RC MEDLINE=22341132; PubMed=12454917;
RX Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
Initiative.";
RT Dev. Dyn. 225:384-391 (2002).

[3]
RN SEQUENCE FROM N.A.
RP TISSUE=Oocytes;
RC Klein S., Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 PDZ/DHR domain.
DR EMBL; BC073110; AAH73110.1; -.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR000798; Ez/rad/moesin.
DR InterPro; IPR003065; FERM.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR011036; PH-related.
DR InterPro; IPR003595; PTPC motif.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00373; Band 41; 1.
DR Pfam; PF00595; PDZ; 1.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00935; BAND41.
DR PRINTS; PR00661; ERMFAMILY.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00295; B41; 1.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00194; PTPC; 1.
DR SMART; SM00404; PTPC motif; 1.
DR PROSITE; PS00660; FERM_1; UNKNOWN_1.
DR PROSITE; PS00057; FERM_3; 1.
DR PROSITE; PS0106; PDZ; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase; Hypothetical protein.
SQ SEQUENCE 920 AA; 105109 MW; 8F0BB89C359CD41E CRC64;

Query Match 40.7%; Score 510; DB 2; Length 920;
Best Local Similarity 43.5%; Pred. No. 2.9e-40;
Matches 104; Conservative 33; Mismatches 88; Indels 14; Gaps 4;

QY 1 QNRDKNRYDILPYDSTRVPLGKKNKYINASYI-----RIVNHEEYFYIATGQPLPE 53
DB 676 QNWDNRKYDVLPYDATRVLLNGEDDYINASYVNMIEPSTNIVNK-----YVATGQLPH 730
QY 54 TIEDFQWQVLENNCNVNIAMITREIECGVIKCYSPISLKEPLEFEHFSVLETFHVTQY 113
DB 731 TCAQFQWQVLEQLSIIIMLTTLTGRTRTKCOQYWP-DPEVWEYKFKRICTEDCTIA 789
QY 114 FTVRVFIQVKSTGKSCQVKHLQTKWPDHGTASADFFIKYVYVRKSHITG-PLLHVC 172

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Db 790 YVREMLLTDTTETGDEPFIHLLQYVWPDHGVDPDSSDFLEFATYVRQKRMENQPVLVHC 849
QY 173 SAGVGRGTGVEICDVVVFSAIEKNYSFDIMNIVTQMRKQRCMIQTKREQYQCYEIVLEV 231
Db 850 SAGIGRTGVLITMETAMCLIEHQVVPVPLDVVRQMRDQRAMMYQTSSQYKFVCEAILR 908

RESULT 8
Q8N4S3 Q8N4S3 PRELIMINARY; PRT; 292 AA.
AC Q8N4S3;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Arimura Y., Hinoda Y., Itoh F., Takekawa M., Tsujisaki M., Adachi M.,
RA Imai K., Yachi A.;
RT "cDNA cloning of new protein tyrosine phosphatases in the human
RT colon.";
RL Tumour Biol. 13:180-186(1992).
[3]
RP SEQUENCE OF 899-913 FROM N.A.
RX MEDLINE=95179278; PubMed=7874267;
RA Ikuta S., Itoh F., Hinoda Y., Toyota M., Makiguchi Y., Imai K.,
RA Yachi A.;
RT "Expression of cytoskeletal-associated protein tyrosine phosphatase
RT PTPH1 mRNA in human hepatocellular carcinoma.";
RL J. Gastroenterol. 29:727-732(1994).
CC -1- FUNCTION: May act at junctions between the membrane and the
CC cytoskeleton.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -1- SIMILARITY: Contains 1 FERM domain.
CC -1- SIMILARITY: Contains 1 PDZ/DHR domain.
-----
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DR EMBL; M64572; AAA35647.1; -
DR EMBL; S39392; AAB22439.2; -
DR EMBL; S76309; AAB33583.1; -
DR PIR; A41109; A41109.
DR HSP; P18031; 1C88.
DR Genew; HGNC:9655; PTPN3.
DR MIM; 176877; -
DR GO; GO:0004725; F:protein-tyrosine-phosphatase activity; TAS.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR000798; Ez/rad/moesin.
DR InterPro; IPR009085; FERM.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR011036; PH related.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00373; Band 41; 1.
DR Pfam; PF00595; PDZ; 1.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00935; BAND41.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00295; B41; 1.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00194; PTPC; 1.

Query Match 39.9%; Score 500; DB 2; Length 292;
Best Local Similarity 42.0%; Pred. No. 6.5e-40;
Matches 102; Conservative 38; Mismatches 85; Indels 18; Gaps 5;

QY 1 QNRDKNRYDILYDSTRVPLGKKNKYNASYI-----RIVNHEEYFYATQGPLPE 53
Db 48 QNLDKRYKDVLPYDITRVLLQGNEDYINASYVNMETPAANLVNK-----YIATQGPLPH 102
QY 54 TIEDEFQWVLENNCNVIMITREICGVKCYSVWPLSLKEPLEFPH--PSVFELETFHVT 111
Db 103 TCAQFQVWVDQKLVLMLVLTUTTERGRTKCHQWTP---DPPDMNHGGPHIQCSBEDCT 159
QY 112 QYFTVRFVQIVKKSQSCQKHLQFTKPDHGTGPASADFFIKYRVYRKSHI-TGPLLV 170
Db 160 IAVSREMLVTNTQTGEHTVTHLQYVWPDHGVDPDSSDFLEFVNVRSRLVDSPEVLV 219
QY 171 HCSAGVGRGTGVEICDVVVFSAIEKNYSFDIMNIVTQMRKQRCMIQTKREQYQCYEIVLE 230
Db 220 HCSAGIGRTGVLVTMETAMCLTERNLPIYPLDVIKRMQRDQAMVQTSQYKFVCEAILR 279
QY 231 VLQ 233
Db 280 VYE 282

RESULT 9
PTN3 HUMAN
ID PTN3_HUMAN STANDARD; PRT; 913 AA.
AC P26045;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 3 (EC 3.1.3.48)
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DE (Protein-tyrosine phosphatase H1) (PTP-H1).
GN Name=PTN3; Synonyms=PTPH1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91296738; PubMed=1648725;
RA Yang Q., Tonks N.K.;
RT "Isolation of a cDNA clone encoding a human protein-tyrosine
RT phosphatase with homology to the cytoskeletal-associated proteins band
RT 4.1, ezrin, and talin.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5949-5953(1991).
[2]
RP SEQUENCE OF 194-896 FROM N.A.
RC TISSUE=Colon;
RA Arimura Y., Hinoda Y., Itoh F., Takekawa M., Tsujisaki M., Adachi M.,
RA Imai K., Yachi A.;
RT "cDNA cloning of new protein tyrosine phosphatases in the human
RT colon.";
RL Tumour Biol. 13:180-186(1992).
[3]
RP SEQUENCE OF 899-913 FROM N.A.
RX MEDLINE=95179278; PubMed=7874267;
RA Ikuta S., Itoh F., Hinoda Y., Toyota M., Makiguchi Y., Imai K.,
RA Yachi A.;
RT "Expression of cytoskeletal-associated protein tyrosine phosphatase
RT PTPH1 mRNA in human hepatocellular carcinoma.";
RL J. Gastroenterol. 29:727-732(1994).
CC -1- FUNCTION: May act at junctions between the membrane and the
CC cytoskeleton.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -1- SIMILARITY: Contains 1 FERM domain.
CC -1- SIMILARITY: Contains 1 PDZ/DHR domain.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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DR EMBL; M64572; AAA35647.1; -
DR EMBL; S39392; AAB22439.2; -
DR EMBL; S76309; AAB33583.1; -
DR PIR; A41109; A41109.
DR HSP; P18031; 1C88.
DR Genew; HGNC:9655; PTPN3.
DR MIM; 176877; -
DR GO; GO:0004725; F:protein-tyrosine-phosphatase activity; TAS.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR000798; Ez/rad/moesin.
DR InterPro; IPR009085; FERM.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR011036; PH related.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00373; Band 41; 1.
DR Pfam; PF00595; PDZ; 1.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00935; BAND41.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00295; B41; 1.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00194; PTPC; 1.
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DR PROSITE; PS00660; FERM 1; 1.
DR PROSITE; PS00661; FERM 2; 1.
DR PROSITE; PS00507; FERM 3; 1.
DR PROSITE; PS00106; PDZ; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Cytoskeleton; Hydrolase; Protein phosphatase; Structural protein.
FT DOMAIN 29 312 FERM.
FT DOMAIN 510 582 PDZ.
FT DOMAIN 670 913 Protein-tyrosine phosphatase.
FT ACT_SITE 842 842 Phosphocysteine intermediate (By similarity).
SQ SEQUENCE 913 AA; 104029 MW; 29A539ACDE2F1515 CRC64;
Query Match 39.8%; Score 499; DB 1; Length 913;
Best Local Similarity 42.0%; Pred. No. 3.3e-39;
Matches 102; Conservative 38; Mismatches 85; Indels 18; Gaps 5;
QY 1 QNRDKRYRDLIPYDSTRVPLGKVKYINASYI-----RIVNHEEYFYIATQGLPE 53
DB 669 QNLNKKRYKQVLPYDTRVLLQGNEDYINASYVNEIIPAANLVNK-----YIATQGLPLH 723
QY 54 TIEDFQWQVLENNCNVIAITREIECGVIRKCYSWPISLKEPLEFEH--FSVFLTEPHVT 111
DB 724 TCAQFQWQVNDKLSLVMLTLTTERGRTKCHQWP---DPPDVNHEGGFHIQCSSEDC 780
QY 112 QYFTRVRFQIVKSKTGKSCQVHLOFTKPDHGTTPASADFFIKYVYVRKSHI--TGPLLV 170
DB 781 IAYVSREMLVTNTQGEHTVTHLYQVAVPDHGPDDSDPFLFVNVRSLRVDSEBVLV 840
QY 171 HCSAGVGRGTGVICVDVVFSAIEKNYSFDIMNIVTOMRKORCGMIQTKEQYQFCYEV 230
DB 841 HCSAGIGRTGLVITMETAMCLTERNLPIYPLDIVRKRDQRMVQTSQYKFVCEAILR 900
QY 231 VLQ 233
DB 901 VYE 903
RESULT 10
Q9WU22 PRELIMINARY; PRT; 926 AA.
AC Q9WU22;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Testis-enriched protein tyrosine phosphatase.
GN Name=Ptpn4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=20510023; PubMed=11054567;
RA Park K.W., Lee E.J., Lee S.H., Lee J.E., Choi E.Y., Kim B.J.,
Hwang R., Park K.A., Baik J.H.;
RT "Molecular cloning and characterization of a protein tyrosine phosphatase enriched in testis, a putative murine homologue of human PTPWEG.";
RT Genes 257:45-55 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Choi E.-Y., Park K.-W., Lee E.-J., Baik J.-H.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 PDZ/DHR domain.
DR EMBL; AF106702; RAD22773.1; --
DR HSSP; P11171; IGG3.
DR MGD; MGI:109792; Ptpn4.
DR GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. .; IDA.

DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR000798; Ez/rad/moesin.
DR InterPro; IPR009065; FERM.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR011036; PH related.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00373; Band 41; 1.
DR Pfam; PF00595; PDZ; 1.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00935; BAND41.
DR PRINTS; PR00661; ERMFAMILY.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00295; B41; 1.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00660; FERM_1; UNKNOWN_1.
DR PROSITE; PS00661; FERM_2; 1.
DR PROSITE; PS00507; FERM_3; 1.
DR PROSITE; PS00106; PDZ; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
SQ SEQUENCE 926 AA; 105713 MW; A344DAD4FF7E2AE2 CRC64;
Query Match 39.4%; Score 493.5; DB 2; Length 926;
Best Local Similarity 41.2%; Pred. No. 1.1e-38;
Matches 101; Conservative 43; Mismatches 80; Indels 21; Gaps 5;
QY 1 QNRDKRYRDLIPYDSTRVPLGKVKYINASYR-----IYNHEEYFYIATQGLPE 53
DB 678 QNISKRYRDISPYDATRVLLKGNEDYINANYINMEIPSSIIINQ-----YIACQGLPH 732
QY 54 TIEDFQWQVLENNCNVIAITREIECGVIRKCYSWPISLKEPLEFEHFSVFLTEPHVTQ- 112
DB 733 TCKDFQWQVLENNCNVIAITREIECGVIRKCYSWPISLKEPLEFEHFSVFLTEPHVTQ- 788
QY 113 --YFTRVRFQIVKSKTGKSCQVHLOFTKPDHGTTPASADFFIKYVYVR--KSHITG 168
DB 789 NPAYIFRKMVLINQEKNESQLTIQYTAMPDGHGVPDDSDFLDFVCHVRDQAGKEPI 848
QY 169 LVHCSAGVGRGTGVICVDVVFSAIEKNYSFDIMNIVTOMRKORCGMIQTKEQYQFCYEV 228
DB 849 IVHCSAGIGRTGLVITMETAMCLTECNQPVYPLDIVRTMRDQRAMMIQTSPQYFVCEAI 908
QY 229 LEVLQ 233
DB 909 LKVE 913
RESULT 11
PTNS_HUMAN STANDARD; PRT; 1948 AA.
ID PTNS_HUMAN Q13332; O75255; O75870; Q15718; Q16341;
AC Q13332; O75255; O75870; Q15718; Q16341;
DT 10-OCT-2003 (Rel. 42, Created)
DT 01-OCT-2004 (Rel. 45, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Receptor-type protein-tyrosine phosphatase S precursor (EC 3.1.3.48) (R-PTP-S) (Protein-tyrosine phosphatase sigma) (R-PTP-sigma).
GN Name=PTPS;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=96102179; PubMed=8524829;
RA Pulido R., Serria-Pages C., Tang M., Streuli M.;
RT "The LAR/PTP delta/PTP sigma subfamily of transmembrane protein-tyrosine-phosphatases: multiple human LAR, PTP delta, and PTP sigma isoforms are expressed in a tissue-specific manner and associate with

RT the LAR-interacting protein LIP.1.1";
RL Proc. Natl. Acad. Sci. U.S.A. 92:11686-11690 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96255038; PubMed=8992885;
RA Endo N., Rutledge S.J., Opas E.E., Vogel R., Rodan G.A., Schmidt A.;
RT "Human protein tyrosine phosphatase-sigma: alternative splicing and
inhibition by bisphosphonates";
RL J. Bone Miner. Res. 11:535-543 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RX PubMed=15057824; DOI=10.1038/nature02399;
RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,
Caenepeel S., Carrano A.V., Caolile C., Chan Y.M., Christensen M.,
Escobar J., Flowers D., Copeland A., Dalin E., Dehal P., Denys M., Dettler J.C.,
Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,
Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,
Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,
Malfatti S., Martinez D., McCreedy P.M., Medina C., Morgan J.,
Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,
Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,
Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,
Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,
Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
Rubin E.M., Lucas S.M.;
RT "The DNA sequence and biology of human chromosome 19";
RL Nature 428:529-535 (2004).
RN [4]
RP SEQUENCE OF 1503-1589 FROM N.A.
RX MEDLINE=92119637; PubMed=1370651;
RA Adachi M., Sekiya M., Arimura Y., Takekawa M., Itoh F., Hinoda Y.,
Imai K., Yachi A.;
RT "Protein-tyrosine phosphatase expression in pre-B cell NALM-6";
RL Cancer Res. 52:737-740 (1992).
RN [5]
RP INTERACTIONS WITH PP2A1; PP2A2 AND PP2A3.
RX MEDLINE=98288299; PubMed=9624153;
RA Serra-Pages C., Medley O.G., Tang M., Hart A., Streuli M.;
RT "Lipins, a family of LAR transmembrane protein-tyrosine phosphatase-
interacting proteins";
RL J. Biol. Chem. 273:15611-15620 (1998).
CC -|- FUNCTION: Interacts with LAR-interacting protein LIP.1.
CC -|- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
tyrosine + phosphate.
CC -|- SUBUNIT: Interacts with PP2A1, PP2A2 and PP2A3.
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=5;
Comment=Additional isoforms seem to exist;
Name=PTPS;
IsoId=Q13332-1; Sequence=Displayed;
Name=PTPS-MEA;
IsoId=Q13332-2; Sequence=VSP_050021;
Name=PTPS-MEB;
IsoId=Q13332-3; Sequence=VSP_050022, VSP_050026, VSP_050027;
Name=PTPS-MEC;
IsoId=Q13332-4; Sequence=VSP_050024;
Name=PTPS-F4-7;
IsoId=Q13332-5; Sequence=VSP_050023, VSP_050025;
CC -|- TISSUE SPECIFICITY: Detected in all tissues tested except for
placenta and liver.
CC -|- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Receptor class 2A subfamily.
CC -|- SIMILARITY: Contains 8 fibronectin type III domains.
CC -|- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -|- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).

DR EMBL; U35234; AAC50239.1; -;
DR EMBL; U40317; AAC50567.1; -;
DR EMBL; AC005790; AAC62832.1; -;
DR EMBL; AC005338; AAC27825.1; -;
DR EMBL; AC005788; AAC62834.1; -;
DR EMBL; S78080; AAE21146.2; -;
DR HSSP; P10586; ILAR.
DR Genew; HGNC:9681; PTPRS.
DR MIM; 601576; -;
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG c2.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 8.
DR Pfam; PF00047; IG; 3.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR0014; FNTYPEIII.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00060; FN3; 8.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS0853; FN3; 8.
DR PROSITE; PS0835; IG LIKE; 3.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS0055; TYR_PHOSPHATASE_PTP; 2.
KW Alternative splicing; Cell adhesion; Glycoprotein; Hydrolase; Signal;
KW Immunoglobulin domain; Protein phosphatase; Receptor; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 29 Potential.
FT CHAIN 30 1948 Receptor-type protein-tyrosine
phosphatase S. (Potential).
FT DOMAIN 30 1282 Extracellular (Potential).
FT TRANSMEM 1283 1303 Potential.
FT DOMAIN 1304 1948 Cytoplasmic (Potential).
FT DOMAIN 33 123 Ig-like C2-type 1.
FT DOMAIN 135 233 Ig-like C2-type 2.
FT DOMAIN 245 327 Ig-like C2-type 3.
FT DOMAIN 332 420 Fibronectin type-III 1.
FT DOMAIN 426 520 Fibronectin type-III 2.
FT DOMAIN 525 614 Fibronectin type-III 3.
FT DOMAIN 618 715 Fibronectin type-III 4.
FT DOMAIN 720 828 Fibronectin type-III 5.
FT DOMAIN 836 923 Fibronectin type-III 6.
FT DOMAIN 928 1031 Fibronectin type-III 7.
FT DOMAIN 1033 1117 Fibronectin type-III 8.
FT DOMAIN 1393 1648 Protein-tyrosine phosphatase 1.
FT DOMAIN 1680 1930 Protein-tyrosine phosphatase 2.
FT DOMAIN 641 644 Poly-Pro.
FT DISULFID 54 107 Potential.
FT DISULFID 156 216 Potential.
FT DISULFID 266 311 Potential.
FT ACT_SITE 1589 1589 Phosphocysteine intermediate (By
similarity).
FT ACT_SITE 1880 1880 Phosphocysteine intermediate (By
similarity).
FT CARBOHYD 263 263 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 308 308 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 733 733 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 940 940 N-linked (GlcNAc. . .) (Potential).
FT VARSPPLIC 190 198 Missing (in isoform PTPS-MEA).


```

[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20219325; PubMed=10754074;
RA Ono-Koyanagi K., Suga H., Katch K., Miyata T.;
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
RT divergence of tissue-specific isoform genes in the early evolution of
RT vertebrates.";
RL J. Mol. Evol. 50:302-311(2000).
[2]
RP SEQUENCE FROM N.A.
RA Ono K.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB033586; BAA95193.1;
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; Tyr_phosphatase.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPc; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
DR Hydrolase.
KW Hydrolase.
FT NON TER
SQ SEQUENCE 468 AA; 53976 MW; 76C975D92D437A86 CRC64;

Query Match 38.7%; Score 485.5; DB 2; Length 468;
Best Local Similarity 41.5%; Pred. No. 2.9e-38;
Matches 100; Conservative 46; Mismatches 80; Indels 15; Gaps 6;

Qy 2 NRDKNRYRDLIPDYSTRVPLG-----KNKDYINASYIRIVNHEEYFYIATQGPLEPTIE 56
Db 225 NKFKNRLVNIMPYETTRVCLQPIRGVSGSDYINASFID--GYRQKAYIATQGELAETTE 282
Qy 57 DFWQMLNLCNVMIATREIECGVIKCYSWPISLKEPLEFHFVSF--LETHVTOYFT 115
Db 283 DFWMLNENSTIVVMTKLREMGREKCHOYWP--AERSARYQYFVDPMAEYNMQYI- 339
Qy 116 VRVFOIVKXSTGKSCQVKHLQFTKWDHGTSPASADFFIKYRVYRKSH---ITGPLLVH 171
Db 340 LREFKVTARDGQSRVTRQFQTDWPEQGVKSGEGFIDFIGQVHKTKHQFGQDGPISVH 399
Qy 172 CSAGVGRGTGVICVDVVFSAIEKNYSFDIMNIVTQMRKQRCMIQTKEQYQFCYEVILEV 231
Db 400 CSAGVGRGTGVITLSIVLERMYEGVVDIFQTVKMLRTQRPAMVQTEDEYQFCYQAALY 459
Qy 232 L 232
Db 460 L 460

RESULT 14
Q9IA18
ID Q9IA18 PRELIMINARY; PRT; 615 AA.
AC Q9IA18;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Receptor protein tyrosine phosphatase CRYP-alpha (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193505; PubMed=10727868;
RA Johnson K.G., Holt C.E.;
RT "Expression of CRYP-alpha, LAR, PTP-delta, and PTP-rho in the
RT developing Xenopus visual system.";
RL Mech. Dev. 92:291-294(2000).

[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20219325; PubMed=10754074;
RA Ono-Koyanagi K., Suga H., Katch K., Miyata T.;
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
RT divergence of tissue-specific isoform genes in the early evolution of
RT vertebrates.";
RL J. Mol. Evol. 50:302-311(2000).
[2]
RP SEQUENCE FROM N.A.
RA Ono K.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB033584; BAA95191.1;
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; Tyr_phosphatase.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPc; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
DR Hydrolase.
KW Hydrolase; Receptor.
FT NON TER
SQ SEQUENCE 615 AA; 70728 MW; 42593554887858AC CRC64;

Query Match 38.7%; Score 485.5; DB 2; Length 615;
Best Local Similarity 41.5%; Pred. No. 4.1e-38;
Matches 100; Conservative 46; Mismatches 80; Indels 15; Gaps 6;

Qy 2 NRDKNRYRDLIPDYSTRVPLG-----KNKDYINASYIRIVNHEEYFYIATQGPLEPTIE 56
Db 372 NKFKNRLVNIMPYETTRVCLQPIRGVSGSDYINASFID--GYRQKAYIATQGELAETTE 429
Qy 57 DFWQMLNLCNVMIATREIECGVIKCYSWPISLKEPLEFHFVSF--LETHVTOYFT 115
Db 430 DFWMLNENSTIVVMTKLREMGREKCHOYWP--AERSARYQYFVDPMAEYNMQYI- 486
Qy 116 VRVFOIVKXSTGKSCQVKHLQFTKWDHGTSPASADFFIKYRVYRKSH---ITGPLLVH 171
Db 487 LREFKVTARDGQSRVTRQFQTDWPEQGVKSGEGFIDFIGQVHKTKHQFGQDGPISVH 546
Qy 172 CSAGVGRGTGVICVDVVFSAIEKNYSFDIMNIVTQMRKQRCMIQTKEQYQFCYEVILEV 231
Db 547 CSAGVGRGTGVITLSIVLERMYEGVVDIFQTVKMLRTQRPAMVQTEDEYQFCYQAALY 606
Qy 232 L 232
Db 607 L 607

RESULT 15
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ID Q9IBA2 PRELIMINARY; PRT; 468 AA.
AC Q9IBA2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RyP2R2Ab protein (fragment).
GN Name=RyP2R2Ab;
OS Potamotrygon motoro (South American freshwater stingray).
OC Eukaryota; Metazoa; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Hyposquala; Pristioraja; Batoida;
OC Myliobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.
OC NCBI_TaxID=86373;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20219325; PubMed=10754074;
RA Ono-Koyanagi K., Suga H., Katch K., Miyata T.;
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
RT divergence of tissue-specific isoform genes in the early evolution of
RT vertebrates.";
RL J. Mol. Evol. 50:302-311(2000).
[2]
RP SEQUENCE FROM N.A.
RA Ono K.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB033584; BAA95191.1;
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
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OM protein - protein search, using sw model

Run on: December 1, 2004, 12:07:42 ; Search time 19.7573 Seconds
(without alignments)
1134.694 Million cell updates/sec

Title: US-09-095-478A-5_COPY_188_420
Perfect score: 1253
Sequence: 1 QNRDKNRYRDLIPYDSTRVP.....MIQTKEQYQFCYEVILEVLQ 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: Pirl:.*
2: pirl:.*
3: pirl:.*
4: pirl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	995	79.4	398	2 T08716	protein-tyrosine-p
2	595.5	47.5	2450	2 S71625	protein-tyrosine-p
3	592.5	47.3	2294	2 I67630	protein-tyrosine-p
4	592.5	47.3	2466	2 I67629	protein-tyrosine-p
5	584.5	46.6	2490	1 A54971	protein-tyrosine-p
6	499	39.8	913	1 A41109	protein-tyrosine-p
7	486.5	38.8	2051	2 T30938	receptor tyrosine
8	476.5	38.0	926	1 A41105	protein-tyrosine-p
9	475	37.9	1337	1 I38670	protein-tyrosine-p
10	474.5	37.9	1501	2 I58148	protein-tyrosine-p
11	474.5	37.9	1907	2 S50893	protein-tyrosine-p
12	474.5	37.9	1912	2 A56178	protein-tyrosine-p
13	471	37.6	1499	2 I50212	protein-tyrosine-p
14	469.5	37.5	1997	1 S12050	protein-tyrosine-p
15	468.5	37.4	1863	2 S46217	protein-tyrosine-p
16	468	37.4	1238	2 S68700	hPTP beta-like tyr
17	468	37.4	1457	1 A48066	protein-tyrosine-p
18	467.5	37.3	583	2 S17671	protein-tyrosine-p
19	463	37.0	597	2 B53978	protein-tyrosine-p
20	463	37.0	694	2 A53978	protein-tyrosine-p
21	463	37.0	1187	1 J44155	protein-tyrosine-p
22	461.5	36.8	1262	1 B48758	protein-tyrosine-p
23	461.5	36.8	1496	1 A48758	protein-tyrosine-p
24	461	36.8	382	1 A38191	protein-tyrosine-p
25	461	36.8	1691	1 D54689	protein-tyrosine-p
26	461	36.8	1894	2 C54689	protein-tyrosine-p
27	460.5	36.8	582	2 A57068	protein-tyrosine-p
28	460.5	36.8	1290	2 A56493	leucocyte common a
29	460.5	36.8	1897	1 TDHULK	leucocyte antigen-

30	460.5	36.8	1898	2 S46216	leucocyte antigen-
31	460	36.7	387	1 A60345	protein-tyrosine-p
32	459	36.6	363	1 S14294	protein-tyrosine-p
33	459	36.6	415	1 A33899	protein-tyrosine-p
34	458.5	36.6	1176	2 I58345	protein-tyrosine-p
35	458	36.6	1452	1 S17669	protein-tyrosine-p
36	457	36.5	1188	1 A57064	protein-tyrosine-p
37	457	36.5	1216	2 S68613	protein-tyrosine-p
38	457	36.5	1452	1 S17670	protein-tyrosine-p
39	456	36.4	405	2 I49372	protein-tyrosine-p
40	454	36.2	1189	1 JC2366	protein-tyrosine-p
41	453	36.2	405	2 S68250	protein-tyrosine-p
42	453	36.2	1187	1 A53661	protein-tyrosine-p
43	452.5	36.1	1175	2 S51005	protein-tyrosine-p
44	451.5	36.0	1174	2 I38140	protein-tyrosine-p
45	450	35.9	356	2 JW0049	protein-tyrosine-p

ALIGNMENTS

RESULT 1

T08716
protein-tyrosine-phosphatase homolog DKFZp566K0524.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08716
R;Ansoerge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16472
A;Accession: T08716
A;Molecule type: mRNA
A;Residues: 1-398 <ANS>
A;Cross-references: UNIPROT:Q9Y406; EMBL:AL050040
A;Experimental source: fetal kidney; clone DKFZp566K0524
C;Genetics:
A;Note: DKFZp566K0524.1
F;161-379/Domain: protein-tyrosine-phosphatase homology <PTP>

Query Match	79.4%	Score	995;	DB	2;	Length	398;
Best Local Similarity	78.0%;	Pred. No.	4.3e-85;				
Matches	181;	Conservative	26;	Mismatches	25;	Indels	0;
Gaps	0;						
QY	2	NRDKNRYRDLIPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGLPETIEDFWQM	61				
Db	161	NREKNRYRDLIPYDSTRVPLGKSKDYINASYIRIVNCGEYFYIATQGLPSTIDDFWQM	220				
QY	62	VLENNCNVIAITREIECGVICKSYWPISLKEPLEFHFVSFLETQYFTVTRVFOI	121				
Db	221	VLENNCNVIAITREIECGVICKSYWPISLKEPLEFHFVSFLETQYFTVTRVFOI	280				
QY	122	VKSTGSKQCVKHLQFTKWPDHGTAPASDFFIKYVRYVRKSHITGPLLHVHCSAGVGRGV	181				
Db	281	VERKSTGSHVQLOFTKWPDHGTAPASDFFIKYVRYVRKSHITGPLLHVHCSAGVGRGV	340				
QY	182	FCVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMQIQKEQYQFCYEVILEVLQ	233				
Db	341	FLCVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMQIQKEQYQFCYEVILEVLQ	392				

RESULT 2

S71625
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 13 - mouse
N;Alternate names: epidermal growth factor-binding protein; serine proteinase
C;Species: Mus musculus (house mouse)
C;Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
C;Accession: S71625; S67987; I81210; I81209; S40290
R;Chida, D.; Kume, T.; Mukoyama, Y.; Tabata, S.; Nomura, N.; Thomas, M.L.; Watanabe, T.
FEBS Lett. 358, 233-239, 1995
A;Title: Characterization of a protein tyrosine phosphatase (RIP) expressed at a very e
A;Reference number: S71625; MUID:95145716; PMID:7843407
A;Accession: S71625
A;Molecule type: mRNA

A;Residues: 1-2450 <CHI>
A;Cross-references: UNIPROT:Q64512; UNIPROT:Q62370; EMBL:D83966; NID:gl232103; PIDN:BAA1
A;Experimental source: strain DBA/2; cell line MEL 745A
R;Wolf, B.B.; Brown, M.D.
FEBS Lett. 376, 177-180, 1995
A;Title: Epidermal growth factor-binding protein activates soluble and receptor-bound si
A;Reference number: S67987; MUID:96105375; PMID:7498536
A;Accession: S67987
A;Molecule type: protein
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1098-1102 <WOL>
A;Experimental source: submaxillary glands
R;Sato, T.; Irie, S.; Kitada, S.; Reed, J.C.
Science 268, 411-415, 1995
A;Title: FAP-1: a protein tyrosine phosphatase that associates with Fas.
A;Reference number: I59595; MUID:95232528; PMID:7536343
A;Accession: I81210
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1329-1354, 'K', 1356-1447, 'R', 1449-1454 <RES>
A;Cross-references: GB:L34582; NID:G806297; PIDN:AAC42056.1; PID:G806298
A;Accession: I81209
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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A;Cross-references: GB:L34581; NID:G806295; PIDN:AAC42055.1; PID:G806296
R;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
submitted to the EMBL Data Library, June 1993
A;Description: Assessment of the expression levels of murine protein-tyrosine phosphatases
A;Reference number: S40280
A;Accession: S40290
A;Molecule type: mRNA
A;Residues: 2266-2372 <HEN>
A;Cross-references: EMBL:Z33059; NID:G438155; PIDN:CAA80594.1; PID:G438156
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A;Gene: Ptpn13
A;Map position: 5
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; transmembrane protein; tyros
F;566-860/Domain: protein 4.1 membrane-binding domain homology <B41>
F;1089-1165/Domain: GLGF domain homology <GLG1>
F;1361-1437/Domain: GLGF domain homology <GLG2>
F;1495-1574/Domain: GLGF domain homology <GLG3>
F;1769-1840/Domain: GLGF domain homology <GLG4>
F;1863-1937/Domain: GLGF domain homology <GLG5>
F;2203-2422/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;2374/Active site: Cys (phosphotyrosine intermediate) #status Predicted
F;2380/Binding site: substrate phosphate (Arg) #status Predicted
Query Match 47.5%; Score 595.5; DB 2; Length 2450;
Best Local Similarity 49.6%; Pred. No. 7.2e-47; Indels 7; Gaps 3;
Matches 117; Conservative 38; Mismatches 74; Indels 7; Gaps 3;
Qy 1 QNRDKRYRDLPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLETIEDFWQ 60
Db 2202 ENRRKNRYKNILPYDTRVPLGDEGGYINATFIRIPVGTQFVYIACQGPLPTTVGVDFWQ 2261
Qy 61 MVLNNCNVIAITREIECGVIKCYSWPISL-KEPFEHFSVLETFHVTQYFTRVP 119
Db 2262 MWVEQNSTVIAMMTQVEGEKIKQRYWPNLSILGTTTANERLRLLALLRMOQLKGFIVRVM 2321
Qy 120 QIVKSTGKSCVKHLQFTKWPDHGTTPASAD---FFIKYRVYRKSHITGPLLHVCAGV 176
Db 2322 ALEDIQTGEVRHISHLNFTAWPDHDTSPQDDLLTFISYMRHRS---GPVITHCSAGI 2378
Qy 177 GRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOKEQYQFCYEIVLEVL 232
Db 2379 GRSGLTICDVVLGLISQLEDFDISLVRCLRHGMVQEGYVFCYQVILYVL 2434
RESULT 3
167630
protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 3 -
C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I67630
R;Maekawa, K.; Inagawa, N.; Nagamatsu, M.; Harada, S.
FEBS Lett. 337, 200-206, 1994
A;Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane
A;Reference number: I53483; MUID:94116679; PMID:8287977
A;Accession: I67630
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2294 <RES>
A;Cross-references: UNIPROT:Q12923; GB:D21211; NID:G452193; PIDN:BAA04752.1; PID:G452194
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
C;Keywords: phosphoric monoester hydrolase
F;574-868/Domain: protein 4.1 membrane-binding domain homology <B41>
F;1182-1258/Domain: GLGF domain homology <GLG2>
F;2046-2285/Domain: protein-tyrosine-phosphatase homology <PTP>
Query Match 47.3%; Score 592.5; DB 2; Length 2294;
Best Local Similarity 47.6%; Pred. No. 1.3e-46; Indels 1; Gaps 1;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;
Qy 1 QNRDKRYRDLPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLETIEDFWQ 60
Db 2045 ENRRKNRYKNILPYDTRVPLGDEGGYINATFIRIPVGTQFVYIACQGPLPTTVGVDFWQ 2104
Qy 61 MVLNNCNVIAITREIECGVIKCYSWPISL-KEPFEHFSVLETFHVTQYFTRVP 119
Db 2105 MIWEQKSTVIAMMTQVEGEKIKQRYWPNLSILGTTTANERLRLLALLRMOQLKGFIVRVM 2164
Qy 120 QIVKSTGKSCVKHLQFTKWPDHGTTPASADFFIKYRVYRKSHITGPLLHVCAGV 179
Db 2165 TLEDIQTGEVRHISHLNFTAWPDHDTSPQDDLLTFISYMRHRSPIITHCSAGIGRS 2224
Qy 180 GVFIQVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOKEQYQFCYEIVLEVL 232
Db 2225 GTLICIDVVLGLISQLEDFDISLVRCLRHGMVQEGYVFCYQVILYVL 2277
RESULT 4
167629
protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 2 -
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I67629
R;Maekawa, K.; Inagawa, N.; Nagamatsu, M.; Harada, S.
FEBS Lett. 337, 200-206, 1994
A;Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membran
A;Reference number: I53483; MUID:94116679; PMID:8287977
A;Accession: I67629
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2466 <RES>
A;Cross-references: UNIPROT:Q12923; GB:D21210; NID:G452191; PIDN:BAA04751.1; PID:G452192
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
C;Keywords: phosphoric monoester hydrolase
F;574-868/Domain: protein 4.1 membrane-binding domain homology <B41>
F;1354-1430/Domain: GLGF domain homology <GLG2>
F;2218-2437/Domain: protein-tyrosine-phosphatase homology <PTP>
Query Match 47.3%; Score 592.5; DB 2; Length 2466;
Best Local Similarity 47.6%; Pred. No. 1.4e-46; Indels 1; Gaps 1;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;
Qy 1 QNRDKRYRDLPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLETIEDFWQ 60
Db 2217 ENRRKNRYKNILPYDTRVPLGDEGGYINATFIRIPVGTQFVYIACQGPLPTTVGVDFWQ 2276
Qy 61 MVLNNCNVIAITREIECGVIKCYSWPISL-KEPFEHFSVLETFHVTQYFTRVP 119
Db 2277 MIWEQKSTVIAMMTQVEGEKIKQRYWPNLSILGTTTANERLRLLALLRMOQLKGFIVRVM 2336
Qy 120 QIVKSTGKSCVKHLQFTKWPDHGTTPASADFFIKYRVYRKSHITGPLLHVCAGV 179
C;Species: Homo sapiens (man)

Db 2337 TLEDIQTRVRIHSHLNTAMPDHTPSQPDLLLTFTISYMRHHSRSPITHTCSAGIGRS 2396

QY 180 GYFICVDVWVFAIEKNSYEDIMNIVTQMRKQRCGMIOQKEQYQFCYEIVLEVL 232
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 2397 GTLICIDVVLGLISQDLDFISDLVRCMRLQRHGMVQTEDQYIFCYQVILYVL 2449

RESULT 5

A54971
protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 1 [V
N;Alternate names: Fas-associated phosphatase FAP-1; protein-tyrosine-phosphatase hPTP1B
C;Species: Homo sapiens (man)
C;Date: 11-Nov-1994 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: A54971; A55114; I59595; I53483; S46955
R;Banville, D.; Ahmad, S.; Stocco, R.; Shen, S.H.
J. Biol. Chem. 269, 22320-22327, 1994
A;Title: A novel protein-tyrosine phosphatase with homology to both the cytoskeletal pro
A;Reference number: A54971; MUID:94350988; PMID:8071359
A;Accession: A54971
A;Molecule type: mRNA
A;Residues: 1-2490 <BAN>
A;Cross-references: UNIPROT:Q12923; GB:U12128
A;Note: Sequence shown follows authors' translation at positions 62-63
R;Saras, J.; Claesson-Welsh, L.; Heldin, C.H.; Gonez, L.J.
J. Biol. Chem. 269, 24082-24089, 1994
A;Title: Cloning and characterization of PTP11, a protein tyrosine phosphatase with simi
A;Reference number: A55114; MUID:95014139; PMID:7929060
A;Accession: A55114
A;Molecule type: mRNA
A;Residues: 1-61, 'GS', 64-839, 'D', 841-1055, 1075-1133, 'EH', 1136-1210, 'I', 1212-1383, 1389-15
A;Cross-references: GB:X80289; NID:9515030; PIDN:CAA56563.1; PID:9515031
R;Sato, T.; Irie, S.; Kitada, S.; Reed, J.C.
Science 268, 411-415, 1995
A;Title: PTP-1: a protein tyrosine phosphatase that associates with Fas.
A;Reference number: I59595; MUID:95232528; PMID:7536343
A;Accession: I59595
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1279-1888 <RES>
A;Cross-references: GB:I34583; NID:G806291; PIDN:AAC41755.1; PID:G806292
R;Maekawa, K.; Inagawa, N.; Nagamatsu, M.; Harada, S.
FEBS Lett. 337, 200-206, 1994
A;Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane
A;Reference number: I53483; MUID:94116679; PMID:8287977
A;Accession: I53483
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-61, 'GS', 64-839, 'D', 841-1210, 'I', 1212-1383, 1389-2299, 'QM', 2302-2490 <RE2>
A;Cross-references: GB:D21209; NID:9452189; PIDN:BA04750.1; PID:9452190
C;Genetics:
A;Gene: GDB:PTPN13
A;Cross-references: GDB:306348; OMIM:600267
A;Map position: 4q21.3-4q21.3
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosi
F;574-868/Domain: protein 4.1 membrane-binding domain homology <B41>
F;1099-1175/Domain: GLGF domain homology <GLG1>
F;1373-1454/Domain: GLGF domain homology <GLG2>
F;1511-1590/Domain: GLGF domain homology <GLG3>
F;1799-1870/Domain: GLGF domain homology <GLG4>
F;1893-1967/Domain: GLGF domain homology <GLG5>
F;2242-2461/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;2413/Active site: Cys [phosphocysteine intermediate] #status predicted
F;2419/Binding site: substrate phosphate (Arg) #status predicted

Query Match 46.6%; Score 584.5; DB 1; Length 2490;
Best Local Similarity 46.8%; Pred. No. 7.8e-46;
Matches 109; Conservative 43; Mismatches 80; Indels 1; Gaps 1;

QY 1 QNRDKNRYRDLPYDSTRVPLGKNKDYINASYIRINWHEEYFYIATQGPLPETIEFWQ 60
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 2241 ENRRKNRYNLLPYDTRVPLGDEGYINASIKIPVSGKEPVIACQGPLPTTVGDWR 2300

QY 61 MVLNENCNVIAITREIEGVKIKSYWPISL-KEPPEHEFHSVFLETHVTQYFVRYV 119
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 2301 VIVEQKSTVIAMNTOVEGEKIKQRYWPNILGKTTWNSRLRLALVRMQOLKGFVVRAM 2360
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 120 QIVKSTGKSCQVKHLQFTKPDHGTASADFFIKYRVVRKSHITGPLLHCSAGVGT 179
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 2361 TLEDIQTRVRIHSHLNTAMPDHTPSQPDLLLTFTISYMRHHSRSPITHTCSAGIGRS 2420

QY 180 GYFICVDVWVFAIEKNSYEDIMNIVTQMRKQRCGMIOQKEQYQFCYEIVLEVL 232
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 2421 GTLICIDVVLGLISQDLDFISDLVRCMRLQRHGMVQTEDQYIFCYQVILYVL 2473

RESULT 6

A41109
protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN3, nonreceptor type 3 [validated] - human
N;Alternate names: PTPH1
C;Species: Homo sapiens (man)
C;Date: 27-Mar-1992 #sequence_revision 02-May-1994 #text_change 09-Jul-2004
C;Accession: A41109; I55698
R;Yang, Q.; Tonks, N.K.
Proc. Natl. Acad. Sci. U.S.A. 88, 5949-5953, 1991
A;Title: Isolation of a cDNA clone encoding a human protein-tyrosine phosphatase with hc
A;Reference number: A41109; MUID:91296738; PMID:1648725
A;Accession: A41109
A;Molecule type: mRNA
A;Residues: 1-913 <YAN>
A;Cross-references: UNIPROT:P26045; GB:M64572; NID:G179912; PIDN:AAA35647.1; PID:G179913
R;Ikuta, S.; Itoh, F.; Hinoda, Y.; Toyota, M.; Makiguchi, Y.; Imai, K.; Yachi, A.
J. Gastroenterol. 29, 727-732, 1994
A;Title: Expression of cytoskeletal-associated protein tyrosine phosphatase PTPH1 mRNA;
A;Reference number: I55698; MUID:95179278; PMID:7874267
A;Accession: I55698
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 899-913 <RES>
A;Cross-references: GB:576309; NID:G913165; PIDN:AAB33583.1; PID:G913166
C;Genetics:
A;Gene: GDB:PTPN3
A;Cross-references: GDB:131386; OMIM:176877
A;Map position: 9q31-9q31
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology;
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphata
F;31-308/Domain: protein 4.1 membrane-binding domain homology <B41>
F;516-590/Domain: GLGF domain homology <GLG>
F;670-890/Domain: protein-tyrosine-phosphatase homology <PTP>
F;842/Active site: Cys [phosphocysteine intermediate] #status predicted
F;848/Binding site: substrate phosphate (Arg) #status predicted

Query Match 39.8%; Score 499; DB 1; Length 913;
Best Local Similarity 42.0%; Pred. No. 2.2e-38;
Matches 102; Conservative 38; Mismatches 85; Indels 18; Gaps 5;

QY 1 QNRDKNRYRDLPYDSTRVPLGKNKDYINASYIRINWHEEYFYIATQGPLPE 53
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 669 QNLDKNRYKDVLPDYTRVLLQGNEDYINASYVNMETPAANLVNK-----YIATQGPLPH 723
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 54 TIEDFWQVLENNCNVIAITREIEGVKIKSYWPISLKEPPEFH--FSVFLETHVT 111
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 724 TCAQFWQVWVDQKLSLVMLTLTERTGRTKCHQWP---DPDVMNHGGFHIQCSSECT 780
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 112 QYFTRVRFQIVKKSQKSCQVKHLQFTKPDHGTASADFFIKYRVVRKSHI-TGPLLV 170
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 781 IAYVSREMLVNTQTGEHTVTHLYQYVWPDHGTGIPDDSSDFLEFVNVRSIRVDSPEVLV 840
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 171 HCSAGVGRGTGVFICVDVWVFAIEKNSYFDIMNIVTQMRKQRCGMIOQKEQYQFCYEIVLE 230
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 841 HCSAGIGTGLVITMETAMCLTERNLPIYPLDIVRKMRDQAMVQTSQYKFCVCEALR 900
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 231 VLQ 233
| :
Db 901 VYE 903

RESULT 7
T30938
receptor tyrosine phosphatase - medicinal leech
C:Species: Hirudo medicinalis (medicinal leech)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30938
R:Gershon, T.R.; Baker, M.; Nitabach, M.; Wu, P.; Macagno, E.R.
submitted to the EMBL Data Library, December 1997
A:Description: Two receptor tyrosine phosphatases of the IAR subfamily are expressed in
A:Reference number: Z20939
A:Accession: T30938
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2051 <GB>
A:Cross-references: UNIPROT:O44328; EMBL:AF017083; NID:g2695654; PID:g2695655; PIDN:AAB9
C:Genetics:
A:Gene: IAR2
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
ogy

Query Match 38.8%; Score 486.5; DB 2; Length 2051;
Best Local Similarity 41.1%; Pred. No. 8.7e-37;
Matches 99; Conservative 45; Mismatches 82; Indels 15; Gaps 6;

QY 2 NRDKNRYRDLIPYDSTRVLPG-----KNKDYINASYIRIVNHEEYFYIATQGPPLPETIE 56
DB 1808 NKQKNRLVNLVLPYETTRVCLQPIRGVGSIDINASFID--GYRYYRAYIATQGPPLPETIE 1865
QY 57 DFWQVLNENNCVMIATREIECGVVKCYSWPISLKEPLFEHFSVP-LETFHVTVQYFT 115
DB 1866 DFWRALWESNCNIIIVMLTKLREMGREMGCHQWYP--SERSARYQYFVVDPLAEYNMQYI- 1922
QY 116 VRVQIVVKSTGKSCQVHLQFTKWDHGTTPASADFFIKYVYVRKSH-----ITGPLLIVH 171
DB 1923 LREFKVTARDGQGRTRQFOLDTWPEQGVSTGDFIDFGTQHTKTEQVQSGPIAVH 1982
QY 172 CSAGVGRGVPCVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIOKEQYFCYVEIVLEV 231
DB 1983 CSAGVGRGVPCVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIOKEQYFCYVEIVLEV 2042
QY 232 L 232
DB 2043 L 2043

RESULT 8
A41105
protein-tyrosine-phosphatase (EC 3.1.1.3.48) PTPN4, nonreceptor type 4 [validated] - human
N:Alternate names: PTPase MBG
C:Species: Homo sapiens (man)
C:Date: 20-Mar-1992 #sequence_revision 02-May-1994 #text_change 09-Jul-2004
C:Accession: A41105
R:Gu, M.; York, J.D.; Marshawsky, I.; Majerus, P.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 5867-5871, 1991
A:Title: Identification, cloning, and expression of a cytosolic megakaryocyte protein-ty
A:Reference number: A41105; MUID:91288564; PMID:1648233
A:Accession: A41105
A:Molecule type: mRNA
A:Residues: 1-926 <GUA>
A:Cross-references: UNIPROT:P29074; GB:M68941; NID:g190747; PIDN:AAA36530.1; PID:g190748
A:Experimental source: megakaryocytes, cell line MBG-10
C:Genetics:
A:Gene: GDB:PTPN4
A:Cross-references: GDB:131387; OMIM:176878
A:Map position: 9q31-9q31
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology; P
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F:31-308/Domain: protein 4.1 membrane-binding domain homology <B41>
F:523-597/Domain: GLGF domain homology <GLG>
F:679-900/Domain: protein-tyrosine-phosphatase homology <PTP>
F:852/Active site: Cys (phosphocysteine intermediate) #status predicted
F:858/Binding site: substrate phosphate (Arg) #status predicted

Query Match 38.0%; Score 476.5; DB 1; Length 926;
Best Local Similarity 40.8%; Pred. No. 2.9e-36;
Matches 100; Conservative 39; Mismatches 85; Indels 21; Gaps 5;

QY 1 QNRDKNRYRDLIPYDSTRVLPGKKNKYINASYIR-----IVNHEEYFYIATQGPPLPE 53
DB 678 QNISKNRYRDLIPYDSTRVLPGKKNKYINASYIR-----IVNHEEYFYIATQGPPLPH 732
QY 54 TIEDFWQVLNENNCVMIATREIECGVVKCYSWPISLKEPLFEHFSVLETFHVTVQY 113
DB 733 TCTDFWQVMTWEGSSMVVMLTTQVERGRVKCHQWYP-----EPTGSSSYGCVQVTCHESEG 788
QY 114 FTWVVFQ---IVKSTGKSCQVHLQFTKWDHGTTPASADFFIKYVYVRKSHI--TCPL 168
DB 789 NTAYIFRMTLNFQEKNESRPLTQIYIAMPDHDGVPDDSDFLDFVCHVRNKRKAGKEPV 848
QY 169 LVHCSAGVGRGVPCVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIOKEQYFCYVEIV 228
DB 849 VVHCSAGIGRTGVLTITMETACMLECQNPVYVPLDIVTRMDRQAMMIQTPTPSQYRFVCEAI 908
QY 229 LEVLQ 233
DB 909 LKVEE 913

RESULT 9
I38670
protein-tyrosine-phosphatase (EC 3.1.1.3.48), receptor type J precursor - human
N:Alternate names: density enhanced phosphatase-1 (DEP-1); protein-tyrosine phosphatase
C:Species: Homo sapiens (man)
C:Date: 01-Mar-1996 #sequence_revision 08-Mar-1996 #text_change 09-Jul-2004
C:Accession: I38670; I52599
R:Ostman, A.; Yang, Q.; Tonks, N.K.
Proc. Natl. Acad. Sci. U.S.A. 91, 9680-9684, 1994
A:Title: Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, is enhanced
A:Reference number: I38670; MUID:95024024; PMID:7937872
A:Accession: I38670
A:Molecule type: mRNA
A:Residues: 1-1337 <RES>
A:Cross-references: UNIPROT:Q12913; EMBL:U10886; NID:G558754; PID:G558755
A:Experimental source: HeLa cells
R:Honda, H.; Inazawa, J.; Nishida, J.; Yazaki, Y.; Hirai, H.
Blood 84, 4186-4194, 1994
A:Title: Molecular cloning, characterization, and chromosomal localization of a novel p
A:Reference number: I52599; MUID:95086212; PMID:7994032
A:Accession: I52599
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-216, 'LTGVKAA', 225-260, 'G', 262-285, 'GTEGGLDASNTSRA', 302, 'S', 304, 'TAPVHD
A:Cross-references: GB:D37781; NID:G633072; PIDN:BA07035.1; PID:G633073
C:Comment: Enhanced expression of this protein with increasing cell density suggests a
C:Genetics:
A:Gene: GDB:PTPRJ
A:Cross-references: GDB:385040; OMIM:600925
A:Map position: 19q13.4-19q13.4
C:Function:
A:Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and
C:Superfamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III repe
C:Keywords: Glycoprotein; phosphoprotein; phosphoric monoester hydrolase; receptor; tra
F:1-35/Domain: signal sequence #status predicted <SIG>
F:36-1337/Product: protein-tyrosine-phosphatase, receptor type J #status predicted <MAT
F:118-197/Domain: fibronectin type III repeat homology <3PNA>
F:206-283/Domain: fibronectin type III repeat homology <3PNA>
F:284-356/Domain: fibronectin type III repeat homology <3PND>
F:365-445/Domain: fibronectin type III repeat homology <3PND>
F:453-530/Domain: fibronectin type III repeat homology <3PNE>
F:539-617/Domain: fibronectin type III repeat homology <3PNE>
F:720-804/Domain: fibronectin type III repeat homology <3PNE>
F:972-988/Domain: transmembrane #status predicted <TMN>
F:1665-1289/Domain: protein-tyrosine-phosphatase homology <PTP>
F:72,82,93,104,142,172,192,231,258,278,351,376,413,431,501,525,536,582,603,
F:1239/Active site: Cys (phosphocysteine intermediate) #status predicted

F;1245/Binding site: substrate phosphate (Arg) #status predicted

Query Match 37.9%; Score 475; DB 1; Length 1337;
 Best Local Similarity 40.7%; Pred. No. 6.1e-36;
 Matches 98; Conservative 48; Mismatches 83; Indels 12; Gaps 5;

QY 1 QNRDKNRYDILPYDSTRVPLG---KNKDYINASYIRIVNHEEYFYIATQGPLPETIE 56
 Db 1064 ENKGKRNINLPYDSTRVPLGSRVLSVQTHSTDDIINANYPGVHSHKD--FIATQGPLNLTLL 1121

QY 57 DFQWVLENNCNVMIATREIECGVIKCYSWPISLKEPFEHFSVLETFHTVQFTV 116
 Db 1122 DFRWVWEKNVYALIMLTCKVEQRTKCEYWP--SKQAQYDGDITVAMTSEIVLPBWTI 1179

QY 117 RVFQIVKSTGKSCQCVKHLQFTKWDHGTTPASADFFIKY---VR-YVRKSHITGPLLHVC 172
 Db 1180 RDTFVKNIQTSSEHPLRQFHTSWPDHGVPDPTDLLINFRYLVRDYMKGQSPSPILVHC 1239

QY 173 SAGVGRGTGVFCVDDVFSAEIKNYSFDIMNIVTQMRKQRCGMLOTKEOYQFCVEIVLEV 232
 Db 1240 SAGVGRGTGFIADRLIYQIENENTVDYGIYVLDLRMHRPLMVQTEDQYVFLNQCVLDIV 1299

QY 233 Q 233
 Db 1300 R 1300

RESULT 10

I58148
 protein-tyrosine-phosphatase (EC 3.1.3.48) 2B, splice form LAR - rat
 N;Alternate names: leukocyte common antigen-related phosphatase
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C;Accession: I58148; S46218
 R;Walton, K.M.; Martelli, K.J.; Kwak, S.P.; Dixon, J.E.; Largent, B.L.
 Neuron 11, 387-400, 1993
 A;Title: A novel receptor-type protein tyrosine phosphatase is expressed during neurogen
 A;Reference number: I58148; MUID:93357030; PMID:8352946
 A;Accession: I58148
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-1501 <WAL>
 A;Cross-references: UNIPROT:Q64605; GB:L19933; NID:G310242; PIDN:AAA42309.1; PID:G310243
 A;Note: in Genbank entry RATTYRPHOS, release 113.0, the source is designated as Rattus n
 R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
 Biochem. J. 302, 39-47, 1994
 A;Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-ph
 A;Reference number: S46216; MUID:94347119; PMID:8068021
 A;Accession: S46218
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-1501 <ZHA>
 A;Cross-references: EMBL:L12329; NID:G294573; PIDN:AAC37657.1; PID:G294574
 A;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
 ogy

C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosi
 F;149-209/Domain: immunoglobulin homology <IMM1>
 F;246-300/Domain: immunoglobulin homology <IMM2>
 F;413-506/Domain: fibronectin type III repeat homology <IMM3>
 F;882-1501/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F;969-1190/Domain: protein-tyrosine-phosphatase homology <PTP1>
 F;1258-1481/Domain: protein-tyrosine-phosphatase homology <PTP2>
 F;1142/Active site: Cys (phosphocysteine intermediate) #link PTP1 #status predicted
 F;1148/Binding site: substrate phosphate (Arg) #link PTP1 #status predicted
 F;1433/Active site: Cys (phosphocysteine intermediate) #link PTP2 #status predicted
 F;1439/Binding site: substrate phosphate (Arg) #link PTP2 #status predicted

Query Match 37.9%; Score 474.5; DB 2; Length 1501;
 Best Local Similarity 41.1%; Pred. No. 7.9e-36;
 Matches 99; Conservative 46; Mismatches 81; Indels 15; Gaps 6;

QY 2 NRDKNRYDILPYDSTRVPLG-----KNKDYINASYIRIVNHEEYFYIATQGPLPETIE 56

Db 1258 NKFKNLVNLPIYESSRVLQPIRGVSGSDYINASFID--GYRQQKAYIATQGPLAETTE 1315
 QY 57 DFQWVLENNCNVMIATREIECGVIKCYSWPISLKEPFEHFSVYF-LETFHTVQYFT 115
 Db 1316 DFRWALWENNSTIVMLTKLRMGREKCHQYWP--AERSARYQYFVVDPMAYNMPQYI- 1372

QY 116 VRVQIVKSTGKSCQCVKHLQFTKWDHGTTPASADFFIKYRVYVRKSH-----ITGPLLVH 171
 Db 1373 LREFKVTDARDGQSRTVROFQFTDWPQGAPKSGEGFIDFIGQVHKTKQFGQDGPISVH 1432

QY 172 CSAGVGRGTGVFCVDDVFSAEIKNYSFDIMNIVTQMRKQRCGMLOTKEOYQFCVEIVLEV 231
 Db 1433 CSAGVGRGTGVFTLSIVLERMYEGVVDIFQTVKVLRTQRPAMVQTEDEYQFCFQAALY 1492

QY 232 L 232
 Db 1493 L 1493

RESULT 11

S50893
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type sigma precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
 C;Accession: S50893; S40281
 R;Wagner, J.; Boerboom, D.; Tremblay, M.L.
 Eur. J. Biochem. 226, 773-782, 1994
 A;Title: Molecular cloning and tissue-specific RNA processing of a murine receptor-type
 A;Reference number: S50893; MUID:95112841; PMID:7529177
 A;Accession: S50893
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1907 <WAG>
 A;Cross-references: UNIPROT:Q64494; EMBL:X82288; NID:G587483; PIDN:CAA57732.1; PID:G5874
 R;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
 Submitted to the EMBL Data Library, June 1993
 A;Description: Assessment of the expression levels of murine protein-tyrosine phosphatas
 A;Reference number: S40280
 A;Accession: S40281
 A;Molecule type: mRNA
 A;Residues: 1441-1501, 'E', 1503-1546 <HEN>
 A;Cross-references: EMBL:223050; NID:G438137; PIDN:CAA80585.1; PID:G438138
 C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
 ogy

C;Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
 F;149-209/Domain: immunoglobulin homology <IMM1>
 F;246-300/Domain: immunoglobulin homology <IMM2>
 F;413-506/Domain: fibronectin type III repeat homology <IMM3>
 F;1288-1907/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F;1375-1596/Domain: protein-tyrosine-phosphatase homology <PTP1>
 F;1664-1887/Domain: protein-tyrosine-phosphatase homology <PTP2>
 F;1548/Active site: Cys (phosphocysteine intermediate) #status predicted
 F;1554/Binding site: substrate phosphate (Arg) #status predicted
 F;1839/Active site: Cys (phosphocysteine intermediate) #status predicted
 F;1845/Binding site: substrate phosphate (Arg) #status predicted

Query Match 37.9%; Score 474.5; DB 2; Length 1907;
 Best Local Similarity 41.1%; Pred. No. 1e-35;
 Matches 99; Conservative 46; Mismatches 81; Indels 15; Gaps 6;

QY 2 NRDKNRYDILPYDSTRVPLG-----KNKDYINASYIRIVNHEEYFYIATQGPLPETIE 56
 Db 1664 NKFKNLVNLPIYESSRVLQPIRGVSGSDYINASFID--GYRQQKAYIATQGPLAETTE 1721

QY 57 DFQWVLENNCNVMIATREIECGVIKCYSWPISLKEPFEHFSVYF-LETFHTVQYFT 115
 Db 1722 DFRWALWENNSTIVMLTKLRMGREKCHQYWP--AERSARYQYFVVDPMAYNMPQYI- 1778

QY 116 VRVQIVKSTGKSCQCVKHLQFTKWDHGTTPASADFFIKYRVYVRKSH-----ITGPLLVH 171
 Db 1779 LREFKVTDARDGQSRTVROFQFTDWPQGAPKSGEGFIDFIGQVHKTKQFGQDGPISVH 1838

57 DFQWMLNCCNVIAMITRETCGVIKCYSWYPISLKPELEFHSVF-LETFPHVTQYFT 115
 1727 DFRWMLWNNSTIVVMLTKLRMGREKCHQYWP--AERSARYQYFVVDPMAEYNMPOYI- 1783
 116 VRVFIQVKKSTGKSCQVKHLOFTKWPDHGTPASADFFIKYVRYVRKSH-----ITGPLLVH 171
 1784 LREFKVTDARDGQSRTRVRFQFTDWPQEQVPKSGEGFIDFIGQVHKTKEQFGQDGPISVH 1843
 172 CSAGVGRGTGVFCVDVWFSIAIEKNYSFDDIMNIVTQMRKORCGMIQTKEQYFCYEIVLEV 231
 1844 CSAGVGRGTGVFTLSIVLERMYEGVVDIFQTVKMLRTQRPAMVQIEDQYQSYRAALEY 1903
 232 L 232
 1904 L 1904
 RESULT 13
 I50212
 protein-tyrosine-phosphatase (EC 3.1.3.48) - chicken
 C:Species: Gallus gallus (Chicken)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C:Accession: I50212
 R:Stoker, A.W.
 Mech. Dev. 46, 201-217, 1994
 A:Title: Isoforms of a novel cell adhesion molecule-like protein tyrosine phosphatase
 A:Reference number: I50212; MUID:95001563; PMID:7918104
 A:Accession: I50212
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1499 <STO>
 A:Cross-references: UNIPROT:Q90815; GB:L32780; NID:G485746; PIDN:AAA64460.1; PFI
 C:Genetics:
 C:Superfamily: Leukocyte antigen-related protein; fibronectin type III repeat h
 og
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific p
 F:148-208/Domain: immunoglobulin homology <IM1>
 F:245-299/Domain: immunoglobulin homology <IM2>
 F:317-399/Domain: fibronectin type III repeat homology <3PR>
 F:781-1499/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:1257-1479/Domain: protein-tyrosine-phosphatase homology <PTP2>
 F:1141/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1147/Binding site: substrate phosphate (Arg) #status predicted
 F:1432/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1438/Binding site: substrate phosphate (Arg) #status predicted
 Query Match 37.6%; Score 471; DB 2; Length 1499;
 Best Local Similarity 41.1%; Pred. No. 1.7e-35;
 Matches 99; Conservative 46; Mismatches 80; Indels 16; Gaps 7
 QY 2 NRDKNYRDIPLVDSTRVPLG-----KNKDYINASYIRIVNHREYFYIATQGPLPETIE 56
 DB 1257 NKFKNLNVIMPYETRVCLQPIRGVSGSYINASFID--GYRQKAYIATQGLAETTE 1314
 QY 57 DFQWMLNCCNVIAMITRETCGVIKCYSWYPISLKPELEFHSVF-LETFPHVTQYFT 115
 DB 1315 DFRWMLWNNSTIVVMLTKLRMGREKCHQYWP--AERSARYQYFVVDPMAEYNMPOYI- 1371
 QY 116 VRVFIQVKKSTGKSCQVKHLOFTKWPDHGTPASADFFIKYVRYVRKSH-----ITGPLLVH 171
 DB 1372 LREFKVTDARDGQSRTRVRFQFTDWPQEQVPKSGEGFIDFIGQVHKTKEQFGQDGPISVH 1433
 QY 172 CSAGVGRGTGVFCVDVWFSIAIEKNYSFDDIMNIVTQMRKORCGMIQTKEQYFCYEIVLEV 231
 DB 1432 CSAGVGRGTGVFTLSIVLERMYEGVVDIFQTVKMLRTQRPAMVQIEDQYQSYRAALEY 1491
 QY 232 L 232
 1491 L 1491

S12050

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type beta precursor - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phosphatase
A:Reference number: S12050; S15818; S15819
C:Accession: S12050; S15818; S15819
R:Kruiger, N.X.; Streuli, M.; Saito, H.
EMBO J. 9, 3241-3252, 1990
A:Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatase
A:Reference number: S12049; MUID:9106018; PMID:2170109
A:Accession: S12050
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1997 <KRU>
A:Cross-references: UNIPROT:P23467; GB:X54131; NID:g35787; PIDN:CAA38066.1; PID:g35788
R:de Vries, L.; Li, R.Y.; Ragab, A.; Ragab-Thomas, J.M.F.; Chap, H.
FEBS Lett. 282, 285-288, 1991
A:Title: Expression of a truncated protein-tyrosine phosphatase mRNA in human lung.
A:Reference number: S15818; MUID:91243813; PMID:1645282
A:Accession: S15818
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1872-1911, 'VHMLQK' <VRI>
A:Accession: S15819
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1872-1997 <VR2>
C:Genetics:
A:Gene: GDB:PTPRB; PTPB
A:Cross-references: GDB:127352; OMIM:176882
A:Map position: 12q15-12q21
C:Superfamily: protein-tyrosine-phosphatase, receptor type beta; fibronectin type III repeat
C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; receptor
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-1997/Product: protein-tyrosine-phosphatase, receptor type beta #status predicted <M>
F;23-1997/Domain: extracellular #status predicted <EXT>
F;1626-1642/Domain: transmembrane #status predicted <TMN>
F;1643-1997/Domain: intracellular #status predicted <INT>
F;1727-1997/Domain: intracellular #status predicted <INT>
F;1904/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1910/Binding site: substrate phosphate (Arg) #status predicted

Query Match 37.5%; Score 469.5; DB 1; Length 1997;
Best Local Similarity 41.2%; Pred. No. 3.2e-35;
Matches 100; Conservative 43; Mismatches 87; Indels 13; Gaps 5;
QY 1 QNRDKNRYRDLPYDSTRVPLGK-----NKDYINASYIRIVNHEEYFYIATQGPLPETI 55
Db 1726 ENRGKRNRYRDLPYDSTRVPLGK-----NKDYINASYIRIVNHEEYFYIATQGPLPETI 1783
QY 56 EDFQWVLENNCNVMIATREIECGVIKCYSWPISLKEPLEFHFHSVFLETHVTQYFT 115
Db 1784 DDFWKMVWQNVHNVMTQCVKEGRVKCDHYWPAF-QDSLYYGDLLQLMSLSVLPWT 1842
QY 116 VRVFOIV-KKSTGKSCQVKHLQFTKPDHGTTPASADFFIKVVR-----YVRKSHITGPLV 170
Db 1843 IREFKICGEQLDAHLIRLHFHYIVWPDHGVPTTQSLQIFVTRVRYINRSPGAGTVV 1902
QY 171 HCSAGVGRGTGVFCVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOQKEQYQFCYEIVLE 230
Db 1903 HCSAGVGRGTGVFCVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOQKEQYQFCYEIVLE 230
QY 231 VLQ 233
Db 1963 VLR 1965

RESULT 15

S46217

protein-tyrosine-phosphatase (EC 3.1.3.48) type sigma precursor - rat
N:Alternate names: leukocyte common antigen-related phosphatase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1995 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S46217; S51174; A49104

R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
Biochem. J. 302, 39-47, 1994

A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-phosphatase
A:Reference number: S46216; MUID:94347119; PMID:8068021
A:Accession: S46217
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1863 <ZHA>
A:Cross-references: UNIPROT:Q54605; EMBL:L11587
R:Goldstein, B.J.
submitted to the EMBL Data Library, February 1993
A:Reference number: S51174
A:Accession: S51174
A:Molecule type: mRNA
A:Residues: 1-1788, 'G', 1790-1863 <GOB>
A:Cross-references: EMBL:L11587; NID:g205134; PIDN:AAC37656.1; PID:g205135
R;Yan, H.; Grossman, A.; Wang, H.; D'Eustachio, P.; Mossie, K.; Musacchio, J.M.; Silven
J. Biol. Chem. 268, 24880-24886, 1993
A:Title: A novel receptor tyrosine phosphatase-sigma that is highly expressed in the ner
A:Reference number: A49104; MUID:94043351; PMID:8227050
A:Accession: A49104
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-596, 'R', 598-603, 'I', 967-1788, 'G', 1790-1863 <YAN>
A:Experimental source: brain
A:Note: sequence extracted from NCBI backbone (NCBIP:139669)
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
ogy

C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyc
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-1863/Product: protein-tyrosine-phosphatase #status predicted <MAT>
F;149-209/Domain: immunoglobulin homology <IMM2>
F;246-300/Domain: immunoglobulin homology <IMM2>
F;318-400/Domain: fibronectin type III repeat homology <FN3A>
F;413-499/Domain: fibronectin type III repeat homology <FN3B>
F;511-592/Domain: fibronectin type III repeat homology <FN3C>
F;1244-1863/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1331-1552/Domain: protein-tyrosine-phosphatase homology <PP1>
F;1504/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1510/Binding site: substrate phosphate (Arg) #status predicted
F;1795/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1801/Binding site: substrate phosphate (Arg) #status predicted

Query Match 37.4%; Score 468.5; DB 2; Length 1863;
Best Local Similarity 40.7%; Pred. No. 3.7e-35;
Matches 98; Conservative 46; Mismatches 82; Indels 15; Gaps 6;
QY 2 NRDKNRYRDLPYDSTRVPLG-----NKDYINASYIRIVNHEEYFYIATQGPLPETI 56
Db 1620 NKFNRNLVNLPPYSGSRVCLQPIRGVSGSDYINASFID--GYRQKAYIATQGPLPETI 1677
QY 57 DFWQWVLENNCNVMIATREIECGVIKCYSWPISLKEPLEFHFHSVF-LETHVTQYFT 115
Db 1678 DFWRALWENNSTIVMLTKLRMGREKCHQWPF--AERSARYQYFVVDPMAYNMQYI- 1734
QY 116 VRVFOIVKSTGKSCQVKHLQFTKPDHGTTPASADFFIKVVRKSH-----ITGPLLVH 171
Db 1735 LREFKVTVDARDGSRVTFQFTDWPQCAPKSGEGFIDFIGVHKTKQFGQDAPISVH 1794
QY 172 CSAGVGRGTGVFCVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOQKEQYQFCYEIVLE 231
Db 1795 CSAGVGRGTGVFCVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOQKEQYQFCYEIVLE 231
QY 232 L 232
Db 1855 L 1855

Search completed: December 1, 2004, 12:17:27
Job time : 20.7573 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 1, 2004, 12:16:33 ; Search time 424.441 Seconds
(without alignments)
195.771 Million cell updates/sec

Title: US-09-095-478A-5_COPY_188_420

Perfect score: 1253

Sequence: 1 QNRDKNRYRILLPYDSTRVP.....MIQTKQYQFCYEVILEVLQ 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1253	100.0	354	10	US-09-095-478-6 Sequence 6, Appli
2	1253	100.0	379	10	US-09-095-478-8 Sequence 8, Appli
3	1253	100.0	426	10	US-09-095-478-1 Sequence 1, Appli
4	1253	100.0	463	10	US-09-095-478-2 Sequence 2, Appli
5	1174	93.7	412	10	US-09-095-478-3 Sequence 3, Appli
6	1003	80.0	420	15	US-10-311-764-4 Sequence 4, Appli
7	668	53.3	122	10	US-09-095-478-4 Sequence 4, Appli
8	598.5	47.8	381	10	US-09-095-478-7 Sequence 7, Appli
9	592.5	47.3	358	10	US-09-095-478-9 Sequence 9, Appli
10	592.5	47.3	1267	14	US-10-060-065-35 Sequence 35, Appli
11	592.5	47.3	1267	14	US-10-059-585-56 Sequence 56, Appli
12	592.5	47.3	2466	14	US-10-177-980-12 Sequence 12, Appli
13	592.5	47.3	2466	17	US-10-795-148-2 Sequence 2, Appli

14 592.5 47.3 2485 9 US-09-802-669-46 Sequence 46, Appli
15 592.5 47.3 2485 15 US-10-619-220-46 Sequence 46, Appli
16 592.5 47.3 2485 16 US-10-408-765A-1349 Sequence 1349, Ap
17 566 45.2 122 10 US-09-095-478-5 Sequence 5, Appli
18 564 45.0 263 15 US-10-087-684-93 Sequence 93, Appli
19 564 45.0 263 15 US-10-218-779-93 Sequence 93, Appli
20 538 42.9 235 15 US-10-087-684-94 Sequence 94, Appli
21 538 42.9 235 15 US-10-218-779-94 Sequence 94, Appli
22 538 42.9 235 15 US-10-072-012-819 Sequence 819, App
23 499 39.8 913 9 US-09-848-294-2 Sequence 2, Appli
24 499 39.8 913 14 US-10-293-231-2 Sequence 2, Appli
25 499 39.8 913 14 US-10-366-547-38 Sequence 38, Appli
26 494 39.4 244 9 US-09-848-294-7 Sequence 7, Appli
27 494 39.4 244 14 US-10-293-231-7 Sequence 7, Appli
28 488.5 39.0 1948 9 US-09-808-602-55 Sequence 55, Appli
29 488.5 39.0 1948 10 US-09-800-198-45 Sequence 45, Appli
30 488 38.9 703 14 US-10-366-547-40 Sequence 40, Appli
31 487 38.9 291 9 US-09-788-626-22 Sequence 22, Appli
32 483.5 38.6 1502 9 US-09-808-602-54 Sequence 54, Appli
33 483.5 38.6 1502 10 US-09-800-198-44 Sequence 44, Appli
34 482.5 38.5 264 14 US-10-245-539-6 Sequence 6, Appli
35 475 37.9 341 16 US-10-723-606-3 Sequence 3, Appli
36 475 37.9 1337 14 US-10-390-501-2 Sequence 2, Appli
37 475 37.9 1337 14 US-10-366-547-42 Sequence 42, Appli
38 475 37.9 1337 14 US-10-366-547-44 Sequence 44, Appli
39 475 37.9 1337 16 US-10-723-606-2 Sequence 2, Appli
40 474.5 37.9 344 16 US-10-408-765A-1670 Sequence 1670, Ap
41 469.5 37.5 312 15 US-10-634-027-6 Sequence 6, Appli
42 469.5 37.5 319 15 US-10-634-027-7 Sequence 7, Appli
43 469.5 37.5 336 15 US-10-634-027-4 Sequence 4, Appli
44 469.5 37.5 1997 10 US-09-909-567B-54 Sequence 54, Appli
45 469.5 37.5 1997 15 US-10-634-027-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-095-478-6
; Sequence 6, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE Suptp05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115

TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8;
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-09-095-478-8

Query Match 100.0%; Score 1253; DB 10; Length 379;
Best Local Similarity 100.0%; Pred. No. 1.6e-125;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNRDKNRYRDLPLPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
DB 143 QNRDKNRYRDLPLPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 202
QY 61 MVLNNCNVIAITREIECGVIKCYSWPISLKEPLEHEHVSFLETHVTQYFTVRVQ 120
DB 203 MVLNNCNVIAITREIECGVIKCYSWPISLKEPLEHEHVSFLETHVTQYFTVRVQ 262
QY 121 IVKSTGSKQCCKHLOFTKWDHGTTPASADFFIKVYRVKSHITGPTLLVHCSAGVGRG 180
DB 263 IVKSTGSKQCCKHLOFTKWDHGTTPASADFFIKVYRVKSHITGPTLLVHCSAGVGRG 322
QY 181 VFICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIOQKEQYFCYEVILEVLQ 233
DB 323 VFICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIOQKEQYFCYEVILEVLQ 375

RESULT 3
US-09-095-478-1
Sequence 1, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPTPOS AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-09-095-478-6

Query Match 100.0%; Score 1253; DB 10; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.4e-125;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNRDKNRYRDLPLPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
DB 118 QNRDKNRYRDLPLPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 177
QY 61 MVLNNCNVIAITREIECGVIKCYSWPISLKEPLEHEHVSFLETHVTQYFTVRVQ 120
DB 178 MVLNNCNVIAITREIECGVIKCYSWPISLKEPLEHEHVSFLETHVTQYFTVRVQ 237
QY 121 IVKSTGSKQCCKHLOFTKWDHGTTPASADFFIKVYRVKSHITGPTLLVHCSAGVGRG 180
DB 238 IVKSTGSKQCCKHLOFTKWDHGTTPASADFFIKVYRVKSHITGPTLLVHCSAGVGRG 297
QY 181 VFICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIOQKEQYFCYEVILEVLQ 233
DB 298 VFICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIOQKEQYFCYEVILEVLQ 350

RESULT 2
US-09-095-478-8
Sequence 8, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPTPOS AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

```
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-09-095-478-1

Query Match 100.0%; Score 1253; DB 10; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.8e-125;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
Db 188 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 247
QY 61 MVLNNCNVIAITREIECGVIKCYSWPISLKEPLEFEHFSVLETFHFVTOYFTVRVFQ 120
Db 248 MVLNNCNVIAITREIECGVIKCYSWPISLKEPLEFEHFSVLETFHFVTOYFTVRVFQ 307
QY 121 IVKSTGSKQCVKHLQFTKWPDHGTTPASADFFIKYVRYVRKSHITGPLLHCHSAGVGRGT 180
Db 308 IVKSTGSKQCVKHLQFTKWPDHGTTPASADFFIKYVRYVRKSHITGPLLHCHSAGVGRGT 367
QY 181 VFICVDVFSIAEKNSYFDMINIVTQMRKQRCGMIOTKEQYQFCYHIVLEVLQ 233
Db 368 VFICVDVFSIAEKNSYFDMINIVTQMRKQRCGMIOTKEQYQFCYHIVLEVLQ 420

RESULT 4
US-09-095-478-2
; Sequence 2, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 463 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-09-095-478-2

Query Match 100.0%; Score 1253; DB 10; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.8e-125;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
Db 188 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 247
QY 61 MVLNNCNVIAITREIECGVIKCYSWPISLKEPLEFEHFSVLETFHFVTOYFTVRVFQ 120
Db 248 MVLNNCNVIAITREIECGVIKCYSWPISLKEPLEFEHFSVLETFHFVTOYFTVRVFQ 307
QY 121 IVKSTGSKQCVKHLQFTKWPDHGTTPASADFFIKYVRYVRKSHITGPLLHCHSAGVGRGT 180
Db 308 IVKSTGSKQCVKHLQFTKWPDHGTTPASADFFIKYVRYVRKSHITGPLLHCHSAGVGRGT 367
QY 181 VFICVDVFSIAEKNSYFDMINIVTQMRKQRCGMIOTKEQYQFCYHIVLEVLQ 233
Db 368 VFICVDVFSIAEKNSYFDMINIVTQMRKQRCGMIOTKEQYQFCYHIVLEVLQ 420

RESULT 5
US-09-095-478-3
; Sequence 3, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 412 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-09-095-478-3
```

Db	183	NREKNRYDILPYDSTRVPLGKSKDYINASYIRIYNCGEYFYIATQGPLSTIDFWQM	242
Qy	62	VLENNCNVIAITREIEGVIKCYSWPISLKEPFEHFSVLETFHTVQYFTVRVFOI	121
Db	243	VLENNCNVIAITREIEGVIKCYSWPISLKEPFEHFSVLETFHTVQYFTVRVFOI	302
Qy	122	VKKSTGKSCQVHLOFTKMPDHGTTPASADFFIKYVRYVRKSHITGPLLHVCSAGVGRGV	181
Db	303	VEKSTGTSVSVKQLQFTKMPDHGTTPASADFFIKYVRYVRKSHITGPLLHVCSAGVGRGV	362
Qy	182	FTICVDVWFSATKNSYFDMINVTOMRKORCGMIQTKQYQCYEVLVLEVLQ	233
Db	363	FLCVDVWFSATKNSYFDMINVTOMRKORCGMIQTKQYQCYEVLVLEVLQ	414
RESULT 7			
US-09-095-478-4			
; Sequence 4, Application US/09095478			
; Publication No. US20030095970A1			
; GENERAL INFORMATION:			
; APPLICANT: PLOWMAN, Gregory			
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE			
; TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND			
; TITLE OF INVENTION: RELATED PRODUCTS AND			
; TITLE OF INVENTION: METHODS			
; NUMBER OF SEQUENCES: 25			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Lyon & Lyon			
; STREET: 633 West Fifth Street			
; CITY: Los Angeles			
; STATE: California			
; COUNTRY: U.S.A.			
; ZIP: 90071-2066			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb			
; MEDIUM TYPE: storage			
; COMPUTER: IBM Compatible			
; OPERATING SYSTEM: IBM P.C. DOS 5.0			
; SOFTWARE: FastSeq for Windows 2.0			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/095,478			
; FILING DATE:			
; CLASSIFICATION:			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER:			
; FILING DATE:			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Warburg, Richard J.			
; REGISTRATION NUMBER: 32,327			
; REFERENCE/DOCKET NUMBER: 224/115			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (213) 489-1600			
; TELEFAX: (213) 955-0440			
; TELEX: 67-3510			
; INFORMATION FOR SEQ ID NO: 4:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 122 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: Peptide			
US-09-095-478-4			
Query Match 53.3%; Score 668; DB 10; Length 122;			
Best Local Similarity 100.0%; Pred. No. 2e-63;			
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	57	DFQWVLENNCNVIAITREIEGVIKCYSWPISLKEPFEHFSVLETFHTVQYFTV	116
Db	1	DFQWVLENNCNVIAITREIEGVIKCYSWPISLKEPFEHFSVLETFHTVQYFTV	60

Qy	1	QNRDKNRYDILPYDSTRVPLGKSKDYINASYIRIYNHHEEYFYIATQGPLPETIEDFWQ	60
Db	188	QNRDKNRYDILPYDSTRVPLGKSKDYINASYIRIYNHHEEYFYIATQGPLPETIEDFWQ	247
Qy	61	MLENNCNVIAITREIEGVIKCYSWPISLKEPFEHFSVLETFHTVQYFTVRVFOI	120
Db	248	MLENNCNVIAITREIEGVIKCYSWPISLKEPFEHFSVLETFHTVQYFTVRVFOI	307
Qy	121	IVKXSTGKSCQVHLOFTKMPDHGTTPASADFFIKYVRYVRKSHITGPLLHVCSAGVGRGV	180
Db	308	IVKXSTGKSCQVHLOFTKMPDHGTTPASADFFIKYVRYVRKSHITGPLLHVCSAGVGRGV	367
Qy	181	VFICVDVWFSATKNSYFDMINVTOMRKORCGMIQTK	218
Db	368	VFICVDVWFSATKNSYFDMINVTOMRKORCGMIQTK	405
RESULT 6			
US-10-311-764-4			
; Sequence 4, Application US/10311764			
; Publication No. US20040023245A1			
; GENERAL INFORMATION:			
; APPLICANT: INCYTE GENOMICS, INC.; AU-YOUNG, Janice K.			
; APPLICANT: BAUGHN, Mariah R.; DING, Li			
; APPLICANT: ELLIOTT, Vicki S.; GANDHI, Aneena R.			
; APPLICANT: GRIFFIN, Jennifer A.; HAFALIA, April J.A.			
; APPLICANT: KEARNEY, Liam; LEE, Ernestine A.			
; APPLICANT: LU, Yan; NGUYEN, Damiel B.			
; APPLICANT: ARVIZU, Chandra S.; RAMKUNAR, Jayalaxmi			
; APPLICANT: REDDY, Roopa M.; SAMJANWALA, Madhusudan M.			
; APPLICANT: STEWART, Elizabeth A.; TANG, Y. Tom			
; APPLICANT: THORNTON, Michael B.; TRIBOULEY, Catherine M.			
; APPLICANT: CHAWLA, Narinder K.; YANG, Junming			
; APPLICANT: YAO, Monique G.; YUE, Henry			
; TITLE OF INVENTION: PROTEIN PHOSPHATASES			
; FILE REFERENCE: PI-0126 USN			
; CURRENT APPLICATION NUMBER: US/10/311,764			
; CURRENT FILING DATE: 2002-12-16			
; PRIOR APPLICATION NUMBER: PCT/US01/19442			
; PRIOR FILING DATE: 2001-06-14			
; PRIOR APPLICATION NUMBER: US 60/212,447			
; PRIOR FILING DATE: 2000-06-16			
; PRIOR APPLICATION NUMBER: US 60/213,746			
; PRIOR FILING DATE: 2000-06-22			
; PRIOR APPLICATION NUMBER: US 60/215,210			
; PRIOR FILING DATE: 2000-06-29			
; PRIOR APPLICATION NUMBER: US 60/216,529			
; PRIOR FILING DATE: 2000-07-06			
; PRIOR APPLICATION NUMBER: US 60/218,080			
; PRIOR FILING DATE: 2000-07-12			
; PRIOR APPLICATION NUMBER: US 60/220,117			
; PRIOR FILING DATE: 2000-07-21			
; NUMBER OF SEQ ID NOS: 18			
; SOFTWARE: PERL Program			
; SEQ ID NO 4			
; LENGTH: 420			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc feature			
; OTHER INFORMATION: Incyte ID No. US20040023245A1 7476861CD1			
US-10-311-764-4			
Query Match 80.0%; Score 1003; DB 15; Length 420;			
Best Local Similarity 78.9%; Pred. No. 1.2e-98;			
Matches 183; Conservative 24; Mismatches 25; Indels 0; Gaps 0;			
Qy	2	NREKNRYDILPYDSTRVPLGKSKDYINASYIRIYNHHEEYFYIATQGPLPETIEDFWQ	61

QY 117 RVFQIVKSTGKSOVKHLOFTKPDHGTTPASADFFIKYVYRKSHITGTPLLVHCSAGV 176
Db 61 RVFQIVKSTGKSOVKHLOFTKPDHGTTPASADFFIKYVYRKSHITGTPLLVHCSAGV 120
QY 177 GR 178
Db 121 GR 122

RESULT 8
US-09-095-478-7
; Sequence 7, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-095-478-7

Query Match 47.8%; Score 598.5; DB 10; Length 381;
Best Local Similarity 50.0%; Pred. No. 2.6e-55;
Matches 118; Conservative 37; Mismatches 74; Indels 7; Gaps 3;
QY 1 QNRDKNRYDILPYDSTRVPLGKKNKYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
Db 144 ENRRKNRYKNILPYDSTRVPLGDEGGYINASFIRIPVGTQEFVYIACQGPLPTTVGDFWQ 203
QY 61 MVLNNCNVIAMTREIECGVIKCYSWPISL-KEPLEFEHFSVFLETHVTOYFTVRVF 119
Db 204 MWVEQNSTVIAMTQVEGEKIKCQRYWNIILGKTTWNSNRLALVRMQQLKGFIVRYM 263
QY 120 QIVKSTGKSOVKHLOFTKPDHGTTPASADFFIKYVYRKSHITGTPLLVHCSAGV 176
Db 264 ALEDIQTEVRHISHLNFTAMPDHTPSQPDLLTFISYMRHRS---GPVITHCSAGI 320

QY 177 GRTGVFCVDVWVPSAIEKKNYSFDIMNIVTQMRKQRCGMIOQKEQYQFCYVEIVLEVL 232
Db 321 GRSGTLICIDVVLGLISQDLEFDISDLVRCMRLORHGMVQTEGQYVFCYQVILYVL 376

RESULT 9
US-09-095-478-9
; Sequence 9, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE SUPTP05 AND
; TITLE OF INVENTION: RELATED PRODUCTS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-095-478-9

Query Match 47.3%; Score 592.5; DB 10; Length 358;
Best Local Similarity 47.6%; Pred. No. 1e-54;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;
QY 1 QNRDKNRYDILPYDSTRVPLGKKNKYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
Db 121 ENRRKNRYKNILPYDSTRVPLGDEGGYINASFIRIPVGTQEFVYIACQGPLPTTVGDFWQ 180
QY 61 MVLNNCNVIAMTREIECGVIKCYSWPISL-KEPLEFEHFSVFLETHVTOYFTVRVF 119
Db 181 MWVEQNSTVIAMTQVEGEKIKCQRYWNIILGKTTWNSNRLALVRMQQLKGFIVRYM 240
QY 120 QIVKSTGKSOVKHLOFTKPDHGTTPASADFFIKYVYRKSHITGTPLLVHCSAGV 179
Db 241 TLEDIQTEVRHISHLNFTAMPDHTPSQPDLLTFISYMRHRS---GPVITHCSAGI 300
QY 180 GVIFICVDVWVPSAIEKKNYSFDIMNIVTQMRKQRCGMIOQKEQYQFCYVEIVLEVL 232

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Db 301 GTLICIDVVLGLISQDLDFDISDLVRCMLQRHGMVQTEDQYIFCYQVILYVL 1353

RESULT 10
US-10-060-065-35
; Sequence 35, Application US/10060065
; Publication No. US20030017480A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-ichi Funahashi
; APPLICANT: Chiaki Senoo
; APPLICANT: Jun-ichi Nezu
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 06501-099002
; CURRENT APPLICATION NUMBER: US/10/060,065
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05061
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 35
; LENGTH: 1267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-065-35

Query Match 47.3%; Score 592.5; DB 14; Length 1267;
Best Local Similarity 47.6%; Pred. No. 5.4e-54;
Matches 111; Conservative 4; Mismatches 80; Indels 1; Gaps 1;

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Qy 61 MVLNNCNVIMITREIECGVIKCYSWPISL-KEPLEFEHFSVLETFHTVQYFTRVF 119
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Db 1078 MIWEQKSTVIAMMTQEVEGEKIKCQRYWPNILGKTTVSNRLRLALVRMQLKGFVVRAM 1137
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Qy 120 QIVKSTGKSCVKHLOFTKWPDRGTASADFFIKYVRYVRKSHITGPLLHVSAGVGR 179
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Qy 180 GVFCICVDVWFAIEKNYSFDMINIVTQMRKQRCGMQTKQYQFCYEIVLEVL 232
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Db 1198 GTLICIDVVLGLISQDLDFDISDLVRCMLQRHGMVQTEDQYIFCYQVILYVL 1250
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RESULT 11
US-10-059-585-56
; Sequence 56, Application US/10059585
; Publication No. US20030082776A1
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; GENERAL INFORMATION:
; APPLICANT: Ota, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059,585
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 1267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-059-585-56

Query Match 47.3%; Score 592.5; DB 14; Length 1267;
Best Local Similarity 47.6%; Pred. No. 5.4e-54;
Matches 111; Conservative 4; Mismatches 80; Indels 1; Gaps 1;

Qy 1 QNRDKNRYDILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1018 ENRKRYKNILPYDATRVPLDGGYINASFIPVKGEEFVYIACQGPLTTVGDFWQ 1077
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Qy 61 MVLNNCNVIMITREIECGVIKCYSWPISL-KEPLEFEHFSVLETFHTVQYFTRVF 119
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Db 1078 MIWEQKSTVIAMMTQEVEGEKIKCQRYWPNILGKTTVSNRLRLALVRMQLKGFVVRAM 1137
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Qy 120 QIVKSTGKSCVKHLOFTKWPDRGTASADFFIKYVRYVRKSHITGPLLHVSAGVGR 179
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Db 1138 TLEDIQREVRHISHLNFTAPDHDTSQPDLLTFISYMRHHSRSPITHCAGIGRS 1197
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Qy 180 GVFCICVDVWFAIEKNYSFDMINIVTQMRKQRCGMQTKQYQFCYEIVLEVL 232
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Db 1198 GTLICIDVVLGLISQDLDFDISDLVRCMLQRHGMVQTEDQYIFCYQVILYVL 1250
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RESULT 12
US-10-177-980-12
; Sequence 12, Application US/10177980
; Publication No. US20030166232A1
; GENERAL INFORMATION:
; APPLICANT: Saras, Jan
; APPLICANT: Franz, Petra
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Hellman, Ulf
; APPLICANT: Genez, Leonel Jorge
; APPLICANT: Heldin, Carl-Henrik
; TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
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; FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/10/177,980
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/080,855
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 08/805,583
; PRIOR FILING DATE: 1997-02-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 2466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-980-12

Query Match 47.3%; Score 592.5; DB 14; Length 2466;
Best Local Similarity 47.6%; Pred. No. 1.3e-53;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;

Qy 1 QNRDKNRYRDLDPYDSTRVPLGKKNKYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
Db 2217 ENRRKNRYKNILPYDATRVPLGDEGGYINASFIPVKGEEFVYIACQGPLTTVGDFWQ 2276
Qy 61 MVLNNNCNVIAMITRETECGVICKSYWPISL-KEPLEFEHFSVLETFHVTQYFTVRVF 119
Db 2277 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTWVSNRLRLALVRMQLKGFVVRAM 2336
Qy 120 QIVKSTGKSCQVXHLQFTKWPDHGTPASADFFIKYVYVRKSHITGPLLWHCSAGVGT 179
Db 2337 TLEDIQTRVHRHSHLNTAWPDHDTSPQDDLLTFISYMRHHRSGPIITHCSAGIGRS 2396
Qy 180 GVFCVDVWFSAEIKNYSFDIMNVTQMRKQRCGMQTKQYQFCYIVLVL 232
Db 2397 GTLICIDVWLGLSQDLDFDISDLVRCMRHQHGMVQTEQYIFCYQVILYVL 2449

RESULT 13
US-10-795-148-2
; Sequence 2, Application US/10795148
; Publication No. US20040224337A1
; GENERAL INFORMATION:
; APPLICANT: FOEHR, ERIK
; APPLICANT: JERICIC, JASNA
; APPLICANT: LORENTE, GUSTAVO A.
; APPLICANT: UREER, ROMAN
; TITLE OF INVENTION: USE OF BIOMOLECULAR TARGETS IN THE
; FILE REFERENCE: AGYT-022
; CURRENT APPLICATION NUMBER: US/10/795,148
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/452,169
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2466
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-795-148-2

Query Match 47.3%; Score 592.5; DB 17; Length 2466;
Best Local Similarity 47.6%; Pred. No. 1.3e-53;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;

Qy 1 QNRDKNRYRDLDPYDSTRVPLGKKNKYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
Db 2217 ENRRKNRYKNILPYDATRVPLGDEGGYINASFIPVKGEEFVYIACQGPLTTVGDFWQ 2276
Qy 61 MVLNNNCNVIAMITRETECGVICKSYWPISL-KEPLEFEHFSVLETFHVTQYFTVRVF 119
Db 2277 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTWVSNRLRLALVRMQLKGFVVRAM 2336
Qy 120 QIVKSTGKSCQVXHLQFTKWPDHGTPASADFFIKYVYVRKSHITGPLLWHCSAGVGT 179

; FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/10/177,980
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/080,855
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 08/805,583
; PRIOR FILING DATE: 1997-02-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 2466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-980-12

Query Match 47.3%; Score 592.5; DB 14; Length 2466;
Best Local Similarity 47.6%; Pred. No. 1.3e-53;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;

Qy 1 QNRDKNRYRDLDPYDSTRVPLGKKNKYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
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Db 2277 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTWVSNRLRLALVRMQLKGFVVRAM 2336
Qy 120 QIVKSTGKSCQVXHLQFTKWPDHGTPASADFFIKYVYVRKSHITGPLLWHCSAGVGT 179
Db 2337 TLEDIQTRVHRHSHLNTAWPDHDTSPQDDLLTFISYMRHHRSGPIITHCSAGIGRS 2396
Qy 180 GVFCVDVWFSAEIKNYSFDIMNVTQMRKQRCGMQTKQYQFCYIVLVL 232
Db 2397 GTLICIDVWLGLSQDLDFDISDLVRCMRHQHGMVQTEQYIFCYQVILYVL 2449

RESULT 14
US-09-802-669-46
; Sequence 46, Application US/09802669
; Patent No. US20020004490A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/09/802,669
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 46
; LENGTH: 2485
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-669-46

Query Match 47.3%; Score 592.5; DB 9; Length 2485;
Best Local Similarity 47.6%; Pred. No. 1.3e-53;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;

Qy 1 QNRDKNRYRDLDPYDSTRVPLGKKNKYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
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Qy 61 MVLNNNCNVIAMITRETECGVICKSYWPISL-KEPLEFEHFSVLETFHVTQYFTVRVF 119
Db 2296 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTWVSNRLRLALVRMQLKGFVVRAM 2355
Qy 120 QIVKSTGKSCQVXHLQFTKWPDHGTPASADFFIKYVYVRKSHITGPLLWHCSAGVGT 179
Db 2356 TLEDIQTRVHRHSHLNTAWPDHDTSPQDDLLTFISYMRHHRSGPIITHCSAGIGRS 2415
Qy 180 GVFCVDVWFSAEIKNYSFDIMNVTQMRKQRCGMQTKQYQFCYIVLVL 232
Db 2416 GTLICIDVWLGLSQDLDFDISDLVRCMRHQHGMVQTEQYIFCYQVILYVL 2468

RESULT 15
US-10-619-220-46
; Sequence 46, Application US/10619220
; Publication No. US20040033979A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/10/619,220
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 09/802,669
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
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; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 46
; LENGTH: 2485
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-619-220-46

Query Match 47.3%; Score 592.5; DB 15; Length 2485;
Best Local Similarity 47.6%; Pred. No. 1.3e-53;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;
Qy 1 QNRDKRYRDLPLVDSTFVPLGKKNKDYINASVYIRIVNHEREFYVIATCGPLPETIEDFWQ 60
Db 2236 ENRRKNRYKNILFYDATRVPLGDEGGYINASFIPVKKEEFVYIACQGLPTTVGDFWQ 2295
Qy 61 MVLNNNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVLETFHVTQYFTVRVF 119
Db 2296 MIWEQKSTVIAMMTQVEGEKIKCORYWPNILGKTTMVSNELRLLALVRMQOLKGFVVRAM 2355
Qy 120 QIVKXSTCKSOCVKHLQFTKWPDHGTPASADFFIKYVYVRKSHITGPLLHVCAGVGR 179
Db 2356 TLEDIQTRVVRHISHLNFTAMPDHDTPSQDDLLTFISYMRHHRSGPIITHCSAGIGRS 2415
Qy 180 GVFLCVDVVFSAIEKNYSFDIMNIVTQMRKORCGMIOTKEOYQFCYEIVLEVL 232
Db 2416 GTLICIDVVLGLISQDLDFDISDLVRCMLQRHGNVQIEDQYIFCYQVILIVL 2468

Search completed: December 1, 2004, 12:52:37
Job time : 425.441 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 1, 2004, 12:07:42 ; Search time 25.2076 Seconds
(without alignments)
612.993 Million cell updates/sec

Title: US-09-095-478a-5_COPY_188_420

Perfect score: 1253
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/prodata/1/1aa/PCITUS COMB pep.*
6: /cgn2_6/prodata/1/1aa/backfiles1 pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	592.5	47.3	2465	2	US-08-596-291-3
2	592.5	47.3	2465	3	US-09-100-804-3
3	592.5	47.3	2466	3	US-09-080-855-12
4	592.5	47.3	2466	4	US-09-566-076-12
5	592.5	47.3	2466	5	PCT-US94-09943-2
6	592.5	47.3	2485	3	US-09-290-640-46
7	592.5	47.3	2485	4	US-09-665-615B-46
8	499	39.8	913	4	US-09-848-294-2
9	494	39.4	244	4	US-09-848-294-7
10	489	39.0	231	2	US-08-446-345-37
11	487	38.9	242	2	US-08-685-992-21
12	487	38.9	242	2	US-09-144-925-21
13	483.5	38.6	1911	1	US-08-348-006B-5
14	483.5	38.6	1911	2	US-08-800-825A-5
15	483.5	38.6	1911	3	US-09-158-657-5
16	483.5	38.6	1911	5	PCT-US94-10166-5
17	476.5	38.0	278	1	US-08-201-697-16
18	475	37.9	1337	3	US-08-854-585-2
19	475	37.9	1337	4	US-09-447-533-2
20	475	37.9	1337	5	PCT-US95-05512-2
21	474.5	37.9	1501	2	US-08-447-464-3
22	474.5	37.9	1501	2	US-08-716-679-3
23	468	37.4	1457	2	US-08-652-971-3
24	468	37.4	1457	2	US-08-449-644-1
25	468	37.4	1457	2	US-08-087-244A-1
26	468	37.4	1457	2	US-08-991-258A-3
27	468	37.4	1457	2	US-08-769-399-3

28 468 37.4 1457 3 US-08-991-953A-3 Sequence 3, Appli
29 466.5 37.2 232 2 US-08-446-345-38 Sequence 38, Appli
30 462 36.9 1439 2 US-08-449-644-2 Sequence 2, Appli
31 462 36.9 1439 2 US-08-087-244A-2 Sequence 2, Appli
32 460.5 36.8 538 4 US-09-743-492A-9 Sequence 9, Appli
33 459 36.6 296 4 US-10-374-539-2 Sequence 2, Appli
34 458 36.6 1452 2 US-08-449-644-8 Sequence 8, Appli
35 458 36.6 1452 2 US-08-087-244A-8 Sequence 8, Appli
36 457 36.5 246 4 US-09-848-294-9 Sequence 9, Appli
37 457 36.5 1188 1 US-08-201-697-4 Sequence 4, Appli
38 457 36.5 1452 2 US-08-652-971-4 Sequence 4, Appli
39 457 36.5 1452 2 US-08-991-258A-4 Sequence 4, Appli
40 457 36.5 1452 2 US-08-769-399-4 Sequence 4, Appli
41 457 36.5 1452 3 US-08-991-953A-4 Sequence 4, Appli
42 456.5 36.4 245 2 US-08-685-992-26 Sequence 26, Appli
43 456.5 36.4 245 2 US-09-144-925-26 Sequence 26, Appli
44 455.5 36.4 254 2 US-08-685-992-14 Sequence 14, Appli
45 455.5 36.4 254 2 US-09-144-925-14 Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-08-596-291-3
; Sequence 3, Application US/08596291
; Patent No. 5821075
; GENERAL INFORMATION:
; APPLICANT: GONEZ, LEONEL JORGE
; APPLICANT: SARAS, JAN
; APPLICANT: CLAESSON-WELSH, LENA
; APPLICANT: HELDIN, CARL-HENRIK
; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/596,291
; FILING DATE: 09-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/115,573
; FILING DATE: 01-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: LO461/7000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; TELEX: 92-1742 EZBKIEL
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2465 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-596-291-3

Query Match 47.3%; Score 592.5; DB 2; Length 2465;
Best Local Similarity 47.6%; Pred. No. 1.2e-60;

Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;
QY 1 QNRDKNRYRDIILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
DB 2216 ENRRKNRYKNILPYDATRVPLGDEGGYINASFYIKIPVKEEFYIACQGPLPTTVGDFWQ 2275
QY 61 MYLENNCNVAMITREIECGVTKCYSPISL-KEPLEFEHFSVLETFHTVQYFVRVF 119
DB 2276 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTWNSNRLALVRMQQLKGFVVRAM 2335
QY 120 QIVKKSQKSCQVKHLQFTKWDHGTGPASADFFIKYRVYVRKSHITGPLLHVCASAGVRT 179
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QY 180 GVFIQVDDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOQKEQYQFCYEIVLEVL 232
DB 2396 GTLICIDVVVLGLISQDLDFDISLVRQMLQRHGMVQTEQYIFCYQVILYVL 2448

RESULT 2

US-09-100-804-3
; Sequence 3, Application US/09100804
; Patent No. 6066472
; GENERAL INFORMATION:
; APPLICANT: GONEZ, LEONEL JORGE
; APPLICANT: SARAS, JAN
; APPLICANT: CLAESON-WELSH, LENA
; APPLICANT: HELDIN, CARL-HENRIK
; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,804
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/596,291
; FILING DATE: 09-AUG-1996
; APPLICATION NUMBER: US 08/115,573
; FILING DATE: 01-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09943
; FILING DATE: 01-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: LO461/7003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2465 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-100-804-3

Query Match 47.3%; Score 592.5; DB 3; Length 2465;

Best Local Similarity 47.6%; Pred. No. 1.2e-60;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;
QY 1 QNRDKNRYRDIILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
DB 2216 ENRRKNRYKNILPYDATRVPLGDEGGYINASFYIKIPVKEEFYIACQGPLPTTVGDFWQ 2275
QY 61 MYLENNCNVAMITREIECGVTKCYSPISL-KEPLEFEHFSVLETFHTVQYFVRVF 119
DB 2276 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTWNSNRLALVRMQQLKGFVVRAM 2335
QY 120 QIVKKSQKSCQVKHLQFTKWDHGTGPASADFFIKYRVYVRKSHITGPLLHVCASAGVRT 179
DB 2336 TLEDIQTRVHRHSHLNTAFPDHDTSPQDDLLTFISYMRHHRSGPIITHCSAGIGRS 2395
QY 180 GVFIQVDDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOQKEQYQFCYEIVLEVL 232
DB 2396 GTLICIDVVVLGLISQDLDFDISLVRQMLQRHGMVQTEQYIFCYQVILYVL 2448

RESULT 3

US-09-080-855-12
; Sequence 12, Application US/09080855A
; Patent No. 6083721
; GENERAL INFORMATION:
; APPLICANT: Saraz, Jan
; APPLICANT: Franz, Petra
; APPLICANT: Aspenstrm, Pontus
; APPLICANT: Hellman, Ulf
; APPLICANT: Genez, Leonel Jorge
; APPLICANT: Heldin, Carl-Henrik
; TITLE OF INVENTION: PARG, A GPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
; FILE REFERENCE: L0461/7030
; CURRENT APPLICATION NUMBER: US/09/080,855A
; CURRENT FILING DATE: 1998-05-18
; EARLIER APPLICATION NUMBER: 08/805,583
; EARLIER FILING DATE: 1997-02-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 2466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-080-855-12

Query Match 47.3%; Score 592.5; DB 3; Length 2466;

Best Local Similarity 47.8%; Pred. No. 1.2e-60;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;
QY 1 QNRDKNRYRDIILPYDSTRVPLGKNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
DB 2217 ENRRKNRYKNILPYDATRVPLGDEGGYINASFYIKIPVKEEFYIACQGPLPTTVGDFWQ 2276
QY 61 MYLENNCNVAMITREIECGVTKCYSPISL-KEPLEFEHFSVLETFHTVQYFVRVF 119
DB 2277 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTWNSNRLALVRMQQLKGFVVRAM 2336
QY 120 QIVKKSQKSCQVKHLQFTKWDHGTGPASADFFIKYRVYVRKSHITGPLLHVCASAGVRT 179
DB 2337 TLEDIQTRVHRHSHLNTAFPDHDTSPQDDLLTFISYMRHHRSGPIITHCSAGIGRS 2396
QY 180 GVFIQVDDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOQKEQYQFCYEIVLEVL 232
DB 2397 GTLICIDVVVLGLISQDLDFDISLVRQMLQRHGMVQTEQYIFCYQVILYVL 2448

RESULT 4

US-09-566-076-12
; Sequence 12, Application US/09566076
; Patent No. 6475775
; GENERAL INFORMATION:
; APPLICANT: Saraz, Jan
; APPLICANT: Franz, Petra

```
APPLICANT: Aspenstrm, Pontus
APPLICANT: Hellman, Ulf
APPLICANT: Gonez, Leonel Jorge
APPLICANT: Heldin, Carl-Henrik
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
FILE REFERENCE: L0461/7030
CURRENT APPLICATION NUMBER: US/09/566,076
EARLIER FILING DATE:
CURRENT FILING DATE:
EARLIER APPLICATION NUMBER: 09/080,855
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 2466
TYPE: PRT
ORGANISM: Homo sapiens
US-09-566-076-12

Query Match 47.3%; Score 592.5; DB 4; Length 2466;
Best Local Similarity 47.6%; Pred. No. 1.2e-60;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;

QY 1 QNRDKNRYRDILPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2217 ENRRKNRYKNILPYDATRVPLGDEGGYINASFIPVGKEEFVYIACQGPLTTVGDWFQ 2276
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 MVLNNCNVIAITREIECGVIKCYSWPISL-KEPFEFEHFSVFLETFHVTQYFTRVF 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2277 MIWEQKSTVIAMTQVEGEKIKCQRYWPNILGKTTWVSNRLRLALVRMQQLKGFVVRAM 2336
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 120 QIVKSTGKSCQVKHLQFTKWPDHGTTPASADFFIKYRVYVRKSHITGPLLHCHSAGVGT 179
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2337 TLEDIQTREVRHISHLNFTAWPDHDTSPQDDLLTFISYMRHHRSGPIITHCSAGIGRS 2396
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 180 GVFCVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOKEQYQFCYEVILEVL 232
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2397 GTLICIDVVLGLISQDLDFDISLVRMQLRQHGVMQVEDQYFCYQVILYVL 2449
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
PCT-US94-09943-2
Sequence 2, Application PC/TUS9409943
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
FILING DATE: 01-SEP-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: TWOMEY, MICHAEL J.
REGISTRATION NUMBER: P-38,349
REFERENCE/DOCKET NUMBER: L0461/7000W0
```

```
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
TELEX: 92-1742 EZEKIEL
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2466 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-09943-2

Query Match 47.3%; Score 592.5; DB 5; Length 2466;
Best Local Similarity 47.6%; Pred. No. 1.2e-60;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;

QY 1 QNRDKNRYRDILPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2217 ENRRKNRYKNILPYDATRVPLGDEGGYINASFIPVGKEEFVYIACQGPLTTVGDWFQ 2276
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 MVLNNCNVIAITREIECGVIKCYSWPISL-KEPFEFEHFSVFLETFHVTQYFTRVF 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2277 MIWEQKSTVIAMTQVEGEKIKCQRYWPNILGKTTWVSNRLRLALVRMQQLKGFVVRAM 2336
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 120 QIVKSTGKSCQVKHLQFTKWPDHGTTPASADFFIKYRVYVRKSHITGPLLHCHSAGVGT 179
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2337 TLEDIQTREVRHISHLNFTAWPDHDTSPQDDLLTFISYMRHHRSGPIITHCSAGIGRS 2396
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 180 GVFCVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOKEQYQFCYEVILEVL 232
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2397 GTLICIDVVLGLISQDLDFDISLVRMQLRQHGVMQVEDQYFCYQVILYVL 2449
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
US-09-290-640-46
Sequence 46, Application US/09290640
Patent No. 6204055
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcussen, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 46
LENGTH: 2485
TYPE: PRT
ORGANISM: Homo sapiens
US-09-290-640-46

Query Match 47.3%; Score 592.5; DB 3; Length 2485;
Best Local Similarity 47.6%; Pred. No. 1.2e-60;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;

QY 1 QNRDKNRYRDILPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPETIEDFWQ 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2236 ENRRKNRYKNILPYDATRVPLGDEGGYINASFIPVGKEEFVYIACQGPLTTVGDWFQ 2295
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 MVLNNCNVIAITREIECGVIKCYSWPISL-KEPFEFEHFSVFLETFHVTQYFTRVF 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2296 MIWEQKSTVIAMTQVEGEKIKCQRYWPNILGKTTWVSNRLRLALVRMQQLKGFVVRAM 2355
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 120 QIVKSTGKSCQVKHLQFTKWPDHGTTPASADFFIKYRVYVRKSHITGPLLHCHSAGVGT 179
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2356 TLEDIQTREVRHISHLNFTAWPDHDTSPQDDLLTFISYMRHHRSGPIITHCSAGIGRS 2415
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 180 GVFCVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIOKEQYQFCYEVILEVL 232
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2416 GTLICIDVVLGLISQDLDFDISLVRMQLRQHGVMQVEDQYFCYQVILYVL 2468
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```

RESULT 7
US-09-665-615B-46
; Sequence 46, Application US/09665615B
; Patent No. 66531133
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Wyatt, Jacqueline
; TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-0502
; CURRENT APPLICATION NUMBER: US/09/665.615B
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 2485
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-665-615B-46

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RESULT 8
US-09-848-294-2
; Sequence 2, Application US/09848294
; Patent No. 6479640
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el
; TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal
; TITLE OF INVENTION: Adhesions and Uses Therefor
; FILE REFERENCE: CSHL90-04F7A
; CURRENT APPLICATION NUMBER: US/09/848,294
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 09/235,251
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 08/759,536
; PRIOR FILING DATE: 1996-12-04
; PRIOR APPLICATION NUMBER: 08/107,420
; PRIOR FILING DATE: 1993-08-16
; PRIOR APPLICATION NUMBER: 07/663,579
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 07/494,036
; PRIOR FILING DATE: 1990-03-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 913
; TYPE: PRT
; ORGANISM: Homosapiens
US-09-848-294-2

```

```

Query Match          39.8%; Score 499; DB 4; Length 913;
Best Local Similarity 42.0%; Pred. No. 3.7e-50;
Matches 102; Conservative 38; Mismatches 85; Indels 18; Gaps 5;

QY 1 QNRDKRYRDLDPDSTRVPLGKNKDYINASYI-----RIVNHEEYFYIATQGLPE 53
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 669 QNLDKRYKDVLPDTRVLLQGNEDYINASYVNMIEIPAANLVNK-----YIATQGLPLH 723
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 54 TIEDFWOMVLNNCNKIAMITREIECGVIKCSYWPISLKEPLEPEH--FSVPLETFHVT 111
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 724 TCAQFQWVWDQKLSLIVMLTTTERGRYKCHQWP---DPPDVNMHGGFHIQCQSEDC 780
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 112 QYFTRVRFQIVKKSCTGKSCQVKHLQFTKWPDHGTPASADFFIKYVYVRKSHI-TGFLIV 170
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 781 IAVSREMLVTNTQTGEHVTVHLQVAMPDHGIPDSSDFLEFVNVYVSLRVDSEPLV 840
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 171 HCSAGVGRGTGVCVDVVFSAIEKNYSFDMINVTOMRKQRCGMIQTKEQYFCYEVILE 230
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 841 HCSAGIGRTGVLVTMETACMLTERNLPIYPLDIVRKMRDQAMVQTSSQYKFCVCEAILR 900
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 231 VLQ 233
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 901 VYE 903
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 9
US-09-848-294-7
; Sequence 7, Application US/09848294
; Patent No. 6479640
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el
; TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal
; TITLE OF INVENTION: Adhesions and Uses Therefor
; FILE REFERENCE: CSHL90-04FZA
; CURRENT APPLICATION NUMBER: US/09/848,294
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 09/235,251
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 08/759,536
; PRIOR FILING DATE: 1996-12-04
; PRIOR APPLICATION NUMBER: 08/107,420
; PRIOR FILING DATE: 1993-08-16
; PRIOR APPLICATION NUMBER: 07/663,579
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 07/494,036
; PRIOR FILING DATE: 1990-03-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homosapiens
US-09-848-294-7

Query Match          39.4%; Score 494; DB 4; Length 244;
Best Local Similarity 41.7%; Pred. No. 2.2e-50;
Matches 101; Conservative 38; Mismatches 85; Indels 18; Gaps 5;

QY 2 NRDKNRYRDLDPDSTRVPLGKNKDYINASYI-----RIVNHEEYFYIATQGLPET 54
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 NLDKNRYKDVLPDTRVLLQGNEDYINASYVNMIEIPAANLVNK-----YIATQGLPHT 55
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 55 IEDFWOMVLNNCNKIAMITREIECGVIKCSYWPISLKEPLEPEH--FSVPLETFHVTQ 112
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 56 CQAQFQWVWDQKLSLIVMLTTTERGRYKCHQWP---DPPDVNMHGGFHIQCQSEDC 112
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 113 YFTVRVFOIVKKSCTGKSCQVKHLQFTKWPDHGTPASADFFIKYVYVRKSHI-TGPLLVH 171
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 113 AVSREMLVTNTQTGEHVTVHLQVAMPDHGIPDSSDFLEFVNVYVSLRVDSEPLVH 172
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 172 CSAGVGRGTGVCVDVVFSAIEKNYSFDMINVTOMRKQRCGMIQTKEQYFCYEVILEV 231
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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Db 173 CSAGIGRTGLVLTMTAMCLTERNLPIYPLDIVRKMRDQRAMMVQTSSQYKFCVCEAIRV 232

Qy 232 LQ 233

Db 233 YE 234

RESULT 10

US-08-446-345-37

Sequence 37, Application US/08446345

Patent No. 5831009

GENERAL INFORMATION:

APPLICANT: Ullrich, Axel

APPLICANT: Moller, Niels P.H.

APPLICANT: Moller, Karin B.

TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE

TITLE OF INVENTION: PHOSPHATASES PTP-D1

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: N.Y.

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446.345

FILING DATE: 22-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/234,440

FILING DATE: 28-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30742

REFERENCE/DOCKET NUMBER: 7683-054

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)790-9090

TELEFAX: (212) 869-8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 231 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-446-345-37

Query Match 39.0%; Score 489; DB 2; Length 231;

Best Local Similarity 42.0%; Pred. No. 7.8e-50;

Matches 100; Conservative 37; Mismatches 83; Indels 18; Gaps 5;

Qy 2 NRDKNRYRDLPLPDSYTRVPLGKNDYINASYI-----RIVNHEEEFYIATQGLPET 54

Db 1 NLDKNRYKQVLPYDTTRVLLQGNEDYINASYVNMIEIPAANLVNK-----YIATQGLPHT 55

Qy 55 IEDFWQVWVLENNCNVMIATREIECGVTKCYSWPISLKEPFEH--FSVFLTEHVTQ 112

Db 56 CAQFWQVWVMDQKLSLVMLTTLTERGTCKHQWP---DPPDVMNHGGPHIQOSEDCTI 112

Qy 113 YFTVRVPIVKKSTGKSCQVKHQLFTKWPDPHGTPASADFFIKYVYVRKSHI-TGPLLHV 171

Db 113 AYVSREMLVTNTQTGEHTVTHLQYVAMPDGHIPDDSSDFLEFVYVRSRVDSEPLVH 172

Qy 172 CSAGVGTGTFICVDVWFSAIEKNYSFDMINIVTOMRKQRCGMIOTKQYQFCYELV 229

Db 173 CSAGIGRTGLVLTMTAMCLTERNLPIYPLDIVRKMRDQRAMMVQTSSQYKFCVCEAIL 230

RESULT 11

US-08-685-992-21

Sequence 21, Application US/08685992

Patent No. 5912138

GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas

APPLICANT: Flint, Andrew J.

TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN

TITLE OF INVENTION: TYROSINE PHOSPHATASES

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/685,992

FILING DATE: 25-JUL-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: CSHL96-03

TELECOMMUNICATION INFORMATION:

TELEPHONE: 781-861-6240

TELEFAX: 781-861-9540

TELEX:

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 242 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-685-992-21

Query Match 38.9%; Score 487; DB 2; Length 242;

Best Local Similarity 41.8%; Pred. No. 1.4e-49;

Matches 102; Conservative 37; Mismatches 79; Indels 26; Gaps 7;

Qy 1 QNRDKNRYRDLPLPDSYTRVPLGKNDYINASYI-----RIVNHEEEFYIATQGLPE 53

Db 11 QNLDKNRYKQVLPYDTTRVLLQGNEDYINASYVNMIEIPAANLVNK-----YIATQGLPEH 65

Qy 54 TIEDFWQVWVLENNCNVMIATREIECGVTKCYSWPISLKEPFEHFSVFLTEHVV--- 110

Db 66 TCAQFWQVWVMDQKLSLVMLTTLTERGTCKHQWP---DPPDVMNHGG-----PHIQCO 117

Qy 111 TQVFTVRVFPQ---IVKSKSTGKSCQVKHQLFTKWPDPHGTPASADFFIKYVYVRKSHI-TGP 167

Db 118 SEDCTIAYVSMVLTNTQTGEHTVTHLQYVAMPDGHIPDDSSDFLEFVYVRSRVDSEP 177

Qy 168 LLVHCSAGVGRGVFCVDVWFSAIEKNYSFDMINIVTOMRKQRCGMIOTKQYQFCYEL 227

Db 178 VLVHCSAGIGRTGLVLTMTAMCLTERNLPIYPLDIVRKMRDQRAMMVQTSSQYKFCVCEA 237

Qy 228 VLEV 231

Db 238 ILRV 241

RESULT 12

US-09-144-925-21
; Sequence 21, Application US/09144925
; Patent No. 5951979
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas
; APPLICANT: Flint, Andrew J.
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02421-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,925
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,992
; FILING DATE: July 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-03Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-144-925-21

Query Match 38.9%; Score 487; DB 2; Length 242;

Best Local Similarity 41.8%; Pred. No. 1.4e-49;
Matches 102; Conservative 37; Mismatches 79; Indels 26; Gaps 7;

QY 1 QNRDKNRYRDLIPYDSTRVPLGKNDYINASYI-----RIVNHEEYFYIATQGPLPE 53
Db 11 QNLNKNRYKDVLPYDTTRVLLOGNDYINASYVNWIEIPANLVK-----YIATQGPLPH 65
QY 54 TIEDFWQVLENNCNVMIATREIECGVIKCYSWPISLKEPLEFHFVSFLETHV--- 110
Db 66 TCAQFWQVVDQKLSLVMLTLTTERGRTKCHOYWP---DPPDVNMHGG-----FHIQCO 117
QY 111 TQYFTVRVFPQ--IVKSKTGSQCVKHLQFTKPDHGTASADFFIKYVRYVRKSH-TGP 167
Db 118 SEDCTIAYVSMVNTNTQTGEENHTVTHLQYVAMPDHGIPDDSDFLFVNYVRSLRVDSEP 177
QY 168 LVLHCSAGVGRGVFTCVDFWFSAEKKNYSFDMIVTQMRKQRCGMIOKQYQFCVBEI 227
Db 178 VLVHCSAGIGRTGLVMTMETANCLTERNLPFLDIVRKMQRORAMVQTSSQYKFCVCEA 237
QY 228 VLEV 231
Db 238 ILRV 241

RESULT 13

US-08-348-006B-5

; Sequence 5, Application US/08348006B
; Patent No. 5658756
; GENERAL INFORMATION:
; APPLICANT: RODAN, GIDEON A.
; APPLICANT: SCHMIDT, AZRIEL
; APPLICANT: RUTLEDGE, SU JANE
; TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. MARK HAND
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,006B
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,032
; FILING DATE: 14-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: HAND, J., MARK
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 189921A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3905
; TELEFAX: 908-594-4720
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1911 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-348-006B-5

Query Match 38.6%; Score 483.5; DB 1; Length 1911;

Best Local Similarity 42.0%; Pred. No. 7.7e-48;
Matches 100; Conservative 44; Mismatches 79; Indels 15; Gaps 6;

QY 5 KNRYRDLIPYDSTRVPLG-----KNKDYINASYIRIVNHEEYFYIATQGPLPETIEDFW 59
Db 1671 KNRLVNIWPESTRVCLQPIRGVSGSDYINASFID--GYRQKAYIATQGPLAETTEDFW 1728
QY 60 QMVLNNCNVMIATREIECGVIKCYSWPISLKEPLEFHFVSF-LETFHTVQYPTVRV 118
Db 1729 RMLWENNSTIVVMLTKLRMGKREKCHOYWP--AERSARYQYFVVDPMAYNMPQXI-LRE 1785
QY 119 FOIVKSKTGSQCVKHLQFTKPDHGTASADFFIKYVRYVRKSH-----ITGPLLVHCSA 174
Db 1786 FAVTDARQGRVTRVQFQFTDMPGQGVKSGGFIIDFIGQVHKTKEQFGQDGPISVHCSA 1845
QY 175 GVGRTGVFCVDFWFSAEKKNYSFDMIVTQMRKQRCGMIOKQYQFCVBEIVLEVL 232
Db 1846 GVGRTGVFTLSIVLERMYEGVVDIFQTVKMLRQRPAMVQTEDEYQFCYQAALEYL 1903

RESULT 14

US-08-800-825A-5
; Sequence 5, Application US/08800825A
; Patent No. 5866397
; GENERAL INFORMATION:
; APPLICANT: RODAN, GIDEON A.
; APPLICANT: SCHMIDT, AZRIEL
; APPLICANT: RUTLEDGE, SU JANE

Search completed: December 1, 2004, 12:18:54
Job time : 27.2076 secs

RESULT 15
US-09-158-657-5
; Sequence 5, Application US/09158657
; Patent No. 6214564
; GENERAL INFORMATION:
; APPLICANT: RODAN, GIDEON A.
; APPLICANT: SCHMIDT, AZRIEL
; APPLICANT: RUTLEDGE, SU JANE
; TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA

RESULT 15
US-09-158-657-5
: Sequence 5, Application US/09158657

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OM protein - protein search, using sw model

Run on: December 1, 2004, 12:07:39 ; Search time 81.7544 Seconds
(without alignments)
1022.379 Million cell updates/sec

Title: US-09-095-478A-5_COPY_188_420

Perfect score: 1253

Sequence: 1 QNPKRNYRDLIDYDSTRP.....MIQTKQYQFCYRIVLEVLQ 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesep 23Sep04: *
1: genesep1980s: *
2: genesep1990s: *
3: genesep2000s: *
4: genesep2001s: *
5: genesep2002s: *
6: genesep2003as: *
7: genesep2003bs: *
8: genesep2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1253	100.0	426	2 AAW89249	Aw89249 Mouse PTP
2	1253	100.0	463	2 AAW89250	Aw89250 Mouse PTP
3	1174	93.7	405	2 AAW89251	Aw89251 Mouse PTP
4	1003	80.0	251	6 AAE37994	Aae37994 Human kin
5	1003	80.0	420	5 AAE14454	Aae14454 Human pro
6	995	79.4	398	5 ABG30845	Abg30845 Human tyr
7	995	79.4	398	7 ADD89795	Add89795 Human DKF
8	995	79.4	409	7 ADE09123	Ade09123 Novel pro
9	995	79.4	508	7 ADE08106	Ade08106 Novel pro
10	995	79.4	561	4 ABG06042	Abg06042 Novel hum
11	941	75.1	412	6 AAE37996	Aae37996 Human kin
12	639	51.0	348	8 ADK71863	Adk71863 Human kin
13	592.5	47.3	766	6 ABU70688	Abu70688 Human adi
14	592.5	47.3	1267	4 AAG67637	Aag67637 Amino aci
15	592.5	47.3	1267	4 AAG67458	Aag67458 Amino aci
16	592.5	47.3	2466	2 AAR71498	Aar71498 Human pro
17	592.5	47.3	2466	2 AAW75999	Aaw75999 Intracell
18	592.5	47.3	2466	3 AAY90272	Aay90272 Human PTP
19	592.5	47.3	2485	3 AAB19343	Aab19343 Amino aci
20	592.5	47.3	2485	7 ADJ59543	Adj59543 Human hea
21	592.5	47.3	2485	8 ADL27685	Adl27685 Human Fap
22	592.5	47.3	2485	8 ADM53457	Adm53457 Human Fas
23	566	45.2	122	2 AAW89252	Aw89252 Rat PTP10
24	538	42.9	235	5 ADI17283	Adi17283 Polypepti
25	514	41.0	1028	8 ADF43232	Adf43232 Mouse PTP

ALIGNMENTS

RESULT 1
AAW89249
ID AAW89249 standard; protein; 426 AA.
XX
AC AAW89249;
XX
DT 10-MAR-1999 (first entry)
XX
DE Mouse PTP05.
XX
KW PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase;
KW type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;
KW neurodegenerative disease; neuronal survival; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease.
XX
OS Mus sp.
XX
PN WO9849317-A2.
XX
PD 05-NOV-1998.
XX
PF 27-APR-1998; 98WO-US008439.
XX
PR 28-APR-1997; 97US-0044428P.
PR 20-MAY-1997; 97US-0047222P.
PR 11-JUN-1997; 97US-0049477P.
PR 11-JUN-1997; 97US-0049756P.
PR 18-JUN-1997; 97US-0049914P.
PR 23-OCT-1997; 97US-0063595P.
XX
PA (SUG-) SUGEN INC.
XX
PI Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;
PI Courtneidge SA, App H, Hui TH;
XX
DR WPI; 1999-009434/01.
DR N-PSDB; AAW81744.
XX
PT New nucleic acid encoding specific protein tyrosine phosphatases - useful
PT for identifying specific modulators for treatment and prevention of
PT cancer and neurodegenerative disease.
XX
PS Claim 2; Page 155-157; 193pp; English.
XX
CC The present invention describes isolated, enriched or purified nucleic
CC acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The
CC present sequence represents mouse PTP05. The above proteins, other than
CC ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify

26 500 39.9 913 8 ADO55173
27 499 39.8 868 8 ADF43234
28 499 39.8 913 2 AAW12522
29 499 39.8 913 2 AAY25156
30 499 39.8 913 5 AAG79333
31 499 39.8 913 7 ADD22982
32 499 39.8 913 7 ADL16189
33 499 39.8 913 8 ADF43230
34 488.5 39.0 1948 7 ADE57117
35 488.5 39.0 1949 7 ADE57117
36 488.5 39.0 1949 7 ADE57121
37 488.5 39.0 1949 7 ADD47019
38 488.5 39.0 1949 7 ADD47015
39 488 38.9 703 7 ADL16191
40 487 38.9 291 4 AAG78282
41 483.5 38.6 1911 2 AAR71726
42 483.5 38.6 1911 2 AAW27225
43 483.5 38.6 1911 2 AAW94027
44 483.5 38.6 1911 4 AAU01459
45 482.5 38.5 1254 8 ADN02662

Ado55173 Protein #
Adf43234 Human PTP
Aaw12522 Protein t
Aay25156 Human PTP
Aag79333 PTPH1. 8/
Add22982 Human pro
Adl16189 Human pro
Adf43230 Human PTP
Ade57117 Human dis
Ade57121 Human pro
Add47019 Human pro
Add47015 Human pro
Aag78282 Human PTP
Aar71726 Human PTP
Aaw27225 Human pro
Aaw94027 Human pro
Aau01459 Human pro
Adn02662 Liver dis

PR 11-JUN-1997; 97US-0049756P.
 PR 18-JUN-1997; 97US-0049914P.
 PR 23-OCT-1997; 97US-0063595P.
 XX (SUGEN-) SUGEN INC.
 XX Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;
 PI Courtneidge SA, App H, Hui TH;
 XX WPI; 1999-009434/01.
 DR N-PSDB; AAV81746.
 XX New nucleic acid encoding specific protein tyrosine phosphatases - useful
 PT for identifying specific modulators for treatment and prevention of
 PT cancer and neurodegenerative disease.
 XX Claim 2; Page 158-160; 193pp; English.
 XX The present invention describes isolated, enriched or purified nucleic
 CC acids encoding PTP04, SAB, PTP05, PTP10, ALP and ALK-7 proteins. The
 CC present sequence represents mouse PTP05. The above proteins, other than
 CC ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify
 CC substances that modulate their activity (i.e. agonists and antagonists,
 CC including NBP) in vivo or in vitro. These substances are used to treat or
 CC prevent diseases associated with abnormal signal transduction pathways
 CC that involve the proteins, particularly cancer (e.g. leukaemia and
 CC lymphoma), while modulators of ALK-7 (which is a type I receptor
 CC serine/threonine kinase) are used to promote neuronal survival,
 CC particularly for treating Alzheimer's, Parkinson's or Huntington's
 CC diseases. Nucleic acid fragments of the polynucleotides encoding the
 CC proteins can be used as probes to identify and clone related sequences;
 CC to detect protein-encoded RNA; to generate transgenic animals and in gene
 CC therapy (optionally after mutation). Ab are used to determine the
 CC proteins
 XX Sequence 405 AA;
 SQ
 Query Match 93.7%; Score 1174; DB 2; Length 405;
 Best Local Similarity 100.0%; Pred. No. 1e-126;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QNRDKNRYRDLIPYDSTRVPLGKNDKYNASYIRIVNHEEYFYIATQGPLPTIEDFWQ 60
 DB 188 QNRDKNRYRDLIPYDSTRVPLGKNDKYNASYIRIVNHEEYFYIATQGPLPTIEDFWQ 247
 QY 61 MVLNNCNVMIATREIECGVVKCYSWPISLKEPLEFEHFSVLETFPHVTFYTVRVFQ 120
 DB 248 MVLNNCNVMIATREIECGVVKCYSWPISLKEPLEFEHFSVLETFPHVTFYTVRVFQ 307
 QY 121 IVKSTGSKQCVKHLQFTKWDHGTTPASADFFIKYRVYRKSHITGTLVHCSAGVGRGTG 180
 DB 308 IVKSTGSKQCVKHLQFTKWDHGTTPASADFFIKYRVYRKSHITGTLVHCSAGVGRGTG 367
 QY 181 VFICVDVVFSAIEKNYSFDMNIIVTQMRKORCGMIQTK 218
 DB 368 VFICVDVVFSAIEKNYSFDMNIIVTQMRKORCGMIQTK 405
 RESULT 4
 AAE37994
 ID AAE37994 standard; protein; 261 AA.
 XX AC
 XX AAE37994;
 XX
 DT 06-NOV-2003 (first entry)
 XX Human kinase and phosphatase (KPP-39) protein.
 DE
 XX Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis;
 XX atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer;
 KW psoriasis; thrombocytopenia; developmental disorder; Reiter's syndrome;
 KW renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease;
 KW neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis;
 KW
 KW autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome;
 KW acquired immune deficiency syndrome; immunosuppressive; Crohn's disease;
 KW neurotic; transgenic; dermatitis; multiple sclerosis; diabetes mellitus;
 KW allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome;
 KW osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological;
 KW gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.
 XX Homo sapiens.
 OS
 XX WO2003050084-A2.
 XX 19-JUN-2003.
 XX 06-DEC-2002; 2002WO-US039126.
 XX 07-DEC-2001; 2001US-0340235P.
 PR 19-DEC-2001; 2001US-0343007P.
 PR 21-DEC-2001; 2001US-0343546P.
 PR 04-FEB-2002; 2002US-0354388P.
 PR 15-FEB-2002; 2002US-0357675P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Kable AE, Chien D, Wilson AD, Swarnakar A, Gorvad AE;
 PI Hafalia AJA, Emerling BM, Ramkumar J, Jin P, Griffin JA, Marquis JP;
 PI Baughn MR, Chawla NK, Lehr-Mason PM, Khare R, Lee S, Hawkins PR;
 PI Becha SD, Lee SY, Sprague WW, Zabarjadian Y;
 XX WPI; 2003-532894/50.
 DR N-PSDB; AAD57366.
 XX New human kinases and phosphatases and polynucleotides, useful for
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
 PT cancer or hepatitis.
 XX Claim 1; Page 242; 282pp; English.
 XX The invention relates to an isolated polypeptide, which is a human kinase
 CC and phosphatase (KPP). KPP agonists and antagonists are useful for
 CC diagnosing, treating or preventing disorders associated with aberrant
 CC expression of KPP, particularly cell proliferative disorders (e.g.
 CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal
 CC nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary
 CC thrombocytopenia or cancer), developmental disorders (e.g. renal tubular
 CC acidosis, anaemia or mental retardation), neurological disorders (e.g.
 CC Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/
 CC inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome,
 CC allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's
 CC disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,
 CC gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome,
 CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
 CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
 CC bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP
 CC is useful in assessing the effects of exogenous compounds on the
 CC expression of nucleic acids and kinases and phosphatases. KPP gene is
 CC useful in gene therapy and for creating transgenic animals to model human
 CC disease. The present sequence is human KPP protein
 XX Sequence 261 AA;
 SQ
 Query Match 80.0%; Score 1003; DB 6; Length 261;
 Best Local Similarity 78.3%; Pred. No. 3.5e-107;
 Matches 183; Conservative 24; Mismatches 25; Indels 0; Gaps 0;
 QY 2 NRDKNRYRDLIPYDSTRVPLGKNDKYNASYIRIVNHEEYFYIATQGPLPTIEDFWQ 61
 DB 24 NREKNRYRDLIPYDSTRVPLGKNDKYNASYIRIVNCGEYFYIATQGPLSTIDDFWQ 83
 QY 62 VLENNCNVMIATREIECGVVKCYSWPISLKEPLEFEHFSVLETFPHVTFYTVRVFQ 121
 DB 84 VLENNCNVMIATREIEGGIKCVHYWVPSLKLPLEKHFVLENYQVILQYFIIRMFQV 143

QY 122 VKKSTGKSCVKKHLOFTKWDHGTGPASADFFIKYRVYRKSHITGPLLHVSAGVGTGV 181
 Db 144 VEKSTGTSVSKVQLQFTKWDHGTGPASADFFIKYRVYRKSHITGPLLHVSAGVGTGV 203
 QY 182 FICVDVVVFAIEKNYSFDIMNVTQMKRCGMIOQKEQYQFCVVEIVLEVLQ 233
 Db 204 FLCVDVVVFAICVKNCSFNIMDIVAQMEQRSGMVQTKQYHFCYDVIIVLEVL 255

RESULT 5
 AAE14454
 ID AAE14454 standard; protein; 420 AA.
 XX
 AC AAE14454;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human protein phosphatase-4.
 XX
 KW Human; protein phosphatase; PP-4; immune system disorder; AIDS; allergy;
 KW neurological disorder; developmental disorder; Alzheimer's disease;
 KW cell proliferative disorder; Huntington's disease; arteriosclerosis;
 KW renal tubular acidosis; gonadal dysgenesis; cancer; adenocarcinoma;
 KW leukaemia; transgenic animal; gene therapy.
 XX
 OS Homo sapiens.
 XX

FH Key Location/Qualifiers
 FT Region 183..411
 FT /note= "Protein-tyrosine phosphatase"
 FT Active-site 340..388
 FT /note= "Tyrosine specific protein phosphatase active
 FT site"
 FT Region 351..363
 FT /note= "Tyr_phosphatase"
 FT Domain 362..379
 FT /label= Transmembrane_domain
 XX W0200196546-A2.
 XX
 XX 20-DEC-2001.
 XX
 XX 14-JUN-2001; 2001WO-US019442.
 XX
 PR 16-JUN-2000; 2000US-0212447P.
 PR 22-JUN-2000; 2000US-0213746P.
 PR 29-JUN-2000; 2000US-0215210P.
 PR 06-JUL-2000; 2000US-0216529P.
 PR 12-JUL-2000; 2000US-0218080P.
 PR 21-JUL-2000; 2000US-0220117P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Au-Young J, Baughn MR, Ding L, Elliott VS, Gandhi AR, Griffin JA;
 PI Hafalia A, Kearney L, Lee EA, Lu Y, Nguyen DB, Patterson C;
 PI Ramkumar J, Reddy R, Sanjanwala MS, Stewart EA, Tang YT, Thornton M;
 PI Tribouley CM, Wallia NK, Yang J, Yao MG, Yue H;
 XX
 DR WPI; 2002-090206/12.
 DR N-PSDB; AAD24022.
 XX
 PT Novel polypeptide, useful for diagnosing, treating or preventing
 PT disorders of growth and development, immune system, neurological and cell
 PT proliferation diseases, comprises cancer protein phosphatase
 PT polypeptides.
 XX
 PS Claim 1; Page 105-106; 116pp; English.
 XX
 XX The present sequence is human protein phosphatase (PP)-4. PP
 CC polynucleotide and polypeptide are useful in the diagnosis, treatment and
 CC prevention of immune system disorders, neurological disorders,
 CC developmental disorders and cell proliferative disorders. Examples of
 CC immune system disorders include acquired immune deficiency syndrome

CC (AIDS), severe combined immunodeficiency disease (SCID), adult
 CC respiratory distress syndrome, allergies, amyloidosis, anaemia, asthma,
 CC atherosclerosis, Crohn's disease, atopic dermatitis, diabetes mellitus,
 CC emphysema, Goodpasture's syndrome, gout, Graves' disease, multiple
 CC sclerosis, myasthenia gravis, myocardial or pericardial inflammation,
 CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
 CC rheumatoid arthritis, Sjogren's syndrome, scleroderma, systemic
 CC sclerosis, trauma; neurological disorders include Alzheimer's disease,
 CC Huntington's disease, dementia, epilepsy, Parkinson's disease, mental
 CC retardation and other developmental disorders of central nervous system
 CC such as Down's syndrome, cerebral palsy, periodic paralysis, mental
 CC disorders including mood, anxiety, and schizophrenic disorders, seasonal
 CC affective disorder such as akathisia, amnesia, catatonias, dyskinesia;
 CC developmental disorders include e.g. renal tubular acidosis. Duchenne and
 CC Becker muscular dystrophy, gonadal dysgenesis, hypothyroidism; cell
 CC proliferative disorders include e.g. actinic keratosis, arteriosclerosis,
 CC atherosclerosis, bursitis, cirrhosis, hepatitis, psoriasis and cancer
 CC including adenocarcinoma, leukaemia. The polypeptide and polynucleotide
 CC are further useful for analysing proteome of a tissue or a cell type, for
 CC screening an agonist/antagonist, a compound that specifically binds to it
 CC or its modulator. The polynucleotide is useful for creating knockin
 CC humanised animals (pigs) or transgenic animals (mice or rats) to model
 CC human disease, for generating a transcript image of a tissue or cell
 CC type, which represents the global pattern of gene expression by a
 CC particular tissue or cell type
 XX
 SQ Sequence 420 AA;

Query Match 80.8%; Score 1003; DB 5; Length 420;
 Best Local Similarity 78.9%; Pred. No. 7e-107;
 Matches 183; Conservative 24; Mismatches 25; Indels 0; Gaps 0;

QY 2 NRDKNYRDLTPYDSTRVPLGKNDYINASYIRVNHHEEYFYATQGPLPEIEDFWQM 61
 Db 183 NREKNRYRDLTPYDSTRVPLGSKSDYINASYIRVNGGEEFYATQGPLSTIDDFWQM 242
 QY 62 VLENNCNVIAITREIECGVICKYSYWPISLKEPFEHFSVLETFTHTVQYFTVRVFI 121
 Db 243 VLENNSNVIAITREIEGGIKCYHYWPISLKEPFEHFSVLETFTHTVQYFTVRVFI 302
 QY 122 VKKSTGKSCVKKHLOFTKWDHGTGPASADFFIKYRVYRKSHITGPLLHVSAGVGTGV 181
 Db 303 VEKSTGTSVSKVQLQFTKWDHGTGPASADFFIKYRVYRKSHITGPLLHVSAGVGTGV 362

QY 182 FICVDVVVFAIEKNYSFDIMNVTQMKRCGMIOQKEQYQFCVVEIVLEVLQ 233
 Db 363 FLCVDVVVFAICVKNCSFNIMDIVAQMEQRSGMVQTKQYHFCYDVIIVLEVL 414

RESULT 6

ABG30845
 ID ABG30845 standard; protein; 398 AA.

XX AC ABG30845;

XX DT 21-OCT-2002 (first entry)

XX DE Human tyrosine phosphatase protein #1.

XX
 KW Human; tyrosine phosphatase; obesity; diabetes; Parkinson's disease;
 KW central nervous system disorder; CNS; cardiovascular disorder; stroke;
 KW chronic obstructive pulmonary disease; cancer; multiple sclerosis;
 KW Alzheimer's disease; Huntington's disease; congestive heart failure;
 KW myocardial infarction; chromosome 10.

XX OS Homo sapiens.

XX PN W0200242435-A2.

XX PD 30-MAY-2002.

XX PF 27-NOV-2001; 2001WO-EP013794.

XX

27-NOV-2000; 2000US-0252912P.
(FARB) BAYER AG.
Zhu Z;
WPI; 2002-575236/61.
N-PSDB; ABK99178.

New human tyrosine phosphatase polypeptide, the regulation of which is useful for treating obesity, diabetes, cardiovascular or central nervous system disorder, chronic obstructive pulmonary disease and cancer.

Claim 25; Fig 2; 145pp; English.

The present invention relates to a new human tyrosine phosphatase polypeptide. The invention is useful for the preparation of a medicament for modulating the activity of human tyrosine phosphatase in a disease such as obesity, diabetes, a central nervous system (CNS) disorder, chronic obstructive pulmonary disease, cardiovascular disorder or cancer. The invention is useful for treating a human tyrosine phosphatase dysfunction related disease, preferably the above mentioned diseases. The invention is useful for treating the above mentioned disorders, where the CNS disorder is selected from Parkinson's disease, multiple sclerosis, stroke, Alzheimer's disease, and Huntington's disease, and the cardiovascular disorder is selected from congestive heart failure and myocardial infarction. The molecules of the invention are useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to disease and abnormalities related to the presence of mutations in the polynucleotide coding the polypeptide of the invention. The present amino acid sequence represents the human tyrosine phosphatase protein #1 of the invention. This sequence is encoded by the human tyrosine phosphatase gene located on chromosome 10

Sequence 398 AA;

Query Match 79.4%; Score 995; DB 5; Length 398;
Best Local Similarity 78.0%; Pred. No. 5.5e-106;
Matches 181; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

QY 2 NRDKRYRDLPYDSTRVLGKNKYINASYIRIWNHEEYFYATQGPLETTEDFWQM 61
Db 161 NREKNRYRDLPYDSTRVLGSKSDYINASYIRIWNCGEEFYATQGPLLSTIDDFWQM 220
QY 62 VLENNCNVIAMTRIECGVKCYSWPLSLKEPEHFSVFLETHTVTQYFVRVFI 121
Db 221 VLENNSNVIAMTRIMEGGIKCYHYWPISLKXPLKLKHFRVLENYQLQYFIIRMFQV 280
QY 122 VKKSTGKSQCXVHLQFTKPWDHGTPASADFFIKYVRYVRKSHITGPTLLVHCAGVGRTGV 181
Db 281 VEKSTGTSHSVKQLQFTKPWDHGTPASADSFIKYIRYARKSHLTGPVMVHCSAGIGRTGV 340
QY 182 FICVDVVFAIEKNVSFDIMNVITOMRKORCMIOCKEQOFCYEIVLEVLIQ 233
Db 341 FLCVDVVFAIVKDCSFMINDIVAQRMRSGMWQTKEQYHFCDVIDVLEVLIR 392

RESULT 7
ADD89795
ID ID ADD89795 standard; protein; 398 AA.
XX XX
AC AC ADD89795;
XX XX
DT DT 29-JAN-2004 (first entry)
XX XX
DE DE Human DKFPZP566K0524 protein SEQ ID NO:10.
XX XX
KW KW cancer associated phosphatase; enzyme; human; cancer; tumour; cytostatic; immunosuppressive; antidiabetic; neuroprotective; antiinflammatory; antiarthritic; antipsoriatic; antiarteriosclerotic; antiinflammatory; vulnary; gynaecological; antitumor; antitumor; antitumor; antitumor; autoimmune disease; diabetes mellitus; hyperproliferative disease; rheumatoid arthritis; psoriasis; atherosclerosis; inflammation; scarring;

Db 341 FLCVDVVFCAIVKDCSFNIMDIVAQMREQRSGMVQTKQYHFCYDVLVLR 392

RESULT 8
ADE09123
ID ADE09123 standard; protein; 409 AA.
XX
AC ADE09123;
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel protein-related contig polypeptide sequence #189.
XX
KW novel gene; novel protein; tissue marker; molecular weight marker;
KW chromosome marker; genetic disorder; contig.
XX
OS Unidentified.
XX
PN WO2003054152-A2.
XX
PD 03-JUL-2003.
XX
PF 10-DEC-2002; 2002WO-US039555.
XX
PR 10-DEC-2001; 2001US-0339739P.
PR 11-DEC-2001; 2001US-0339453P.
PR 14-MAR-2002; 2002US-0365091P.
PR 14-MAR-2002; 2002US-0365384P.
PR 12-APR-2002; 2002US-0372381P.
PR 12-APR-2002; 2002US-0372615P.
PR 22-APR-2002; 2002US-00128558.
PR 24-APR-2002; 2002US-0376045P.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX
DR WPI; 2003-569235/53.
XX
PT New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.
XX
PS Disclosure; SEQ ID NO 2667; 1177pp; English.
XX
CC The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present amino acid sequence was used in the
CC exemplification of the invention.
XX
SQ Sequence 409 AA;
Query Match 79.4%; Score 995; DB 7; Length 409;
Best Local Similarity 78.0%; Pred. No. 5.7e-106;
Matches 181; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

QY 2 NRDKNRYRDLIPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPFIETDFWQM 61
Db 172 NREKNRYRDLIPYDSTRVPLGSKDYINASYIRIVNCGEEFYIATQGPLLSTIDDFWQM 231

QY 62 VLENNCNVIAMITRETECGVICKYSWPISLKPLEPHEFSVLETFHVTQYTVRVFOI 121
Db 232 VLENNCNVIAMITREMEGGIKCYHYWPISLKPLELKHFRVPLENYQILQYFIIRMFQV 291

QY 122 VKSTGKSCQVKHLOFTKWDHGTGPASADFFIKYVRVRKSHITGTLVHCSAGVGTGV 181
Db 292 VEKSTGTSVHVKLOFTKWDHGTGPASADSFIKYIRYARKSHLTGPMVHCSAGIGRTGV 351

QY 182 FICVDVVFSALEKNYSFDIMNIVTOMRKQSCMIQTKQYQFCVETVLEVLQ 233
Db 352 FLCVDVVFCAIVKDCSFNIMDIVAQMREQRSGMVQTKQYHFCYDVLVLR 403

RESULT 9
ADE08106
ID ADE08106 standard; protein; 508 AA.
XX
AC ADE08106;
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel protein (useful for identifying genetic disorders) #261.
XX
KW novel gene; novel protein; tissue marker; molecular weight marker;
KW chromosome marker; genetic disorder.
XX
OS Unidentified.
XX
PN WO2003054152-A2.
XX
PD 03-JUL-2003.
XX
PF 10-DEC-2002; 2002WO-US039555.
XX
PR 10-DEC-2001; 2001US-0339739P.
PR 11-DEC-2001; 2001US-0339453P.
PR 14-MAR-2002; 2002US-0365091P.
PR 14-MAR-2002; 2002US-0365384P.
PR 12-APR-2002; 2002US-0372381P.
PR 12-APR-2002; 2002US-0372615P.
PR 22-APR-2002; 2002US-00128558.
PR 24-APR-2002; 2002US-0376045P.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX
DR WPI; 2003-569235/53.
DR N-PSDB; ADE07195.
XX
PT New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.
XX
PS Claim 20; SEQ ID NO 1172; 1177pp; English.
XX
CC The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present amino acid sequence represents a protein
CC of the invention.
XX
SQ Sequence 508 AA;
Query Match 79.4%; Score 995; DB 7; Length 508;
Best Local Similarity 78.0%; Pred. No. 7.8e-106;
Matches 181; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

QY 2 NRDKNRYRDLIPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPFIETDFWQM 61
Db 271 NREKNRYRDLIPYDSTRVPLGSKDYINASYIRIVNCGEEFYIATQGPLLSTIDDFWQM 330

QY 62 VLENNCNVIAMITRETECGVICKYSWPISLKPLEPHEFSVLETFHVTQYTVRVFOI 121
Db 331 VLENNCNVIAMITREMEGGIKCYHYWPISLKPLELKHFRVPLENYQILQYFIIRMFQV 390

Best Local Similarity 78.0%; Pred. No. 9e-106;
Matches 181; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

QY 2 NRDKNRYDILPYDSTRVPLGKNDYINASYIRIVNHEEEVFIATOGPLPETIEDFWQM 61
Db 324 NREKNRYDILPYDSTRVPLGKNDYINASYIRIVNCGEEYFIATOGPLSTIDDFWQM 383

QY 62 VLENNCNVIAMITRETCGVKICVSWPIISLKEPLEFEHFSVLETFHTVQYFTVRVFOI 121
Db 384 VLENNCNVIAMITREMEGGIICVHYWPIISLKKPLELKHFRVPLENYQIQLQYFIIRMFV 443

QY 122 VKSTGKSCQVKHLQFTKWDHGTTPASADFFIKYRVVRKSHITGPLLHCHSAGVGTGV 181
Db 444 VEKSTGTSVSKQLQFTKWDHGTTPASADSFIKYIRVARKSHLTGPMVHCHSAGIGRTGV 503

QY 182 FICVDVVFSAIEKNYSFDIMNIVTQMKQKGMIOQKEQYQFCYEIVLEVLQ 233
Db 504 FLCVDVVFCAIVKDCSFNIMDIVAQMREQRSGMVQTKRQHFVCFYDVLVLR 555

RESULT 11
AAE37996
ID AAE37996 standard; protein; 412 AA.
XX AC AAE37996;
XX DT 06-NOV-2003 (first entry)
XX DE Human kinase and phosphatase (KPP-41) protein.
XX KW Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis;
KW atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer;
KW psoriasis; thrombocytopaenia; developmental disorder; Reiter's syndrome;
KW renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease;
KW neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis;
KW autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome;
KW acquired immune deficiency syndrome; immunosuppressive; Crohn's disease;
KW neutropenic; transgenic; dermatitis; multiple sclerosis; diabetes mellitus;
KW allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome;
KW osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological;
KW gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.
XX OS Homo sapiens.
XX PN WO2003050084-A2.
XX PD 19-JUN-2003.
XX PF 06-DEC-2002; 2002WO-US039126.
XX PR 07-DEC-2001; 2001US-0340235P.
XX PR 19-DEC-2001; 2001US-0343007P.
XX PR 21-DEC-2001; 2001US-0343546P.
XX PR 04-FEB-2002; 2002US-0354388P.
XX PR 15-FEB-2002; 2002US-0357675P.
XX PA (INCY-) INCYTE GENOMICS INC.
XX PI Kable AE, Chien D, Wilson AD, Swarnakar A, Corvad AE;
PI Hafalia AJA, Emerling BM, Ramkumar J, Jin P, Griffin JA, Marquis JP;
PI Baughn MR, Chawla NK, Lehr-Mason PM, Khare R, Lee S, Hawkins PR;
PI Becha SD, Lee SY, Sprague WW, Zebajadian Y;
XX DR WPI; 2003-532894/50.
XX DR N-PSDB; AAD57368.
XX PR New human kinases and phosphatases and polynucleotides, useful for
XX PT diagnosing, treating or preventing autoimmune or inflammatory disorders
XX PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
XX PT cancer or hepatitis.
XX PS Claim 1; Page 243-244; 282pp; English.
XX

QY 122 VKSTGKSCQVKHLQFTKWDHGTTPASADFFIKYRVVRKSHITGPLLHCHSAGVGTGV 181
Db 391 VEKSTGTSVSKQLQFTKWDHGTTPASADSFIKYIRVARKSHLTGPMVHCHSAGIGRTGV 450

QY 182 FICVDVVFSAIEKNYSFDIMNIVTQMKQKGMIOQKEQYQFCYEIVLEVLQ 233
Db 451 FLCVDVVFCAIVKDCSFNIMDIVAQMREQRSGMVQTKRQHFVCFYDVLVLR 502

RESULT 10
ABG06042
ID ABG06042 standard; protein; 561 AA.
XX AC ABG06042;
XX DT 13-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #6033.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX DR N-PSDB; AAS70229.
XX PR New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX PS Claim 20; SEQ ID NO 36401; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful for treating disorders
CC of sites expressing (II). (I) and (II) are useful for biological activity. The
CC involving aberrant protein expression or biological activities in
CC polypeptide and polynucleotide sequences have applications of mutations
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG0377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: the sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 561 AA;
Query Match 79.4%; Score 995; DB 4; Length 561;

CC The invention relates to an isolated polypeptide, which is a human kinase
 CC and phosphatase (KPP). KPP agonists and antagonists are useful for
 CC diagnosing, treating or preventing disorders associated with aberrant
 CC expression of KPP, particularly cell proliferative disorders (e.g.
 CC arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal
 CC nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary
 CC thrombocytopaenia or cancer), developmental disorders (eg. renal tubular
 CC acidosis, anaemia or mental retardation), neurological disorders (e.g.
 CC Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/
 CC inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome,
 CC allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's
 CC disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,
 CC gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome,
 CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
 CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
 CC bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP
 CC is useful in assessing the effects of exogenous compounds on the
 CC expression of nucleic acids and kinases and phosphatases. KPP gene is
 CC useful in gene therapy and for creating transgenic animals to model human
 CC disease. The present sequence is human KPP protein
 XX
 SQ Sequence 412 AA;

Query Match 75.1%; Score 941; DB 6; Length 412;
 Best Local Similarity 78.9%; Pred. No. 1e-99;
 Matches 172; Conservative 22; Mismatches 24; Indels 0; Gaps 0;
 QY 2 NRDKNRYDILPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPFIEDFWQM 61
 Db 183 NREKNRYDILPYDSTRVPLGSKNDYINASYIRIVNCGEYFYIATQGPLSTIDFWQM 242
 QY 62 VLENNCNVMIATREIECGVVKCYSWPISLKEPFEHFSVLETFHVTQYFTVRVFOI 121
 Db 243 VLENNCNVMIATREIEGGIKCYHWYPISLKPLKHFVLENYQILQYFIIRMFQV 302
 QY 122 VKSTGSKQCVKHLQFTKPDHGTTPASADFFIKYVRYVRKSHITGPLLHVCSSAGVGTGV 181
 Db 303 VKSTGTSVSKQLQFTKPDHGTTPASADFFIKYIRYARKSHULTGPMVHCSAGIGRTGV 362
 QY 182 FICVDVWFSAIEKNYSFDMINIVTOMRKORCGMIQKE 219
 Db 363 FLCVDVWFCAIVKNCSEFNMDIVAQMRQSGMWQTK 400

RESULT 12
 ADK71863
 ID ADK71863 standard; protein; 348 AA.
 AC ADK71863;

XX 20-MAY-2004 (first entry)

XX Human kinase and phosphatase KPP-40 protein.

XX human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic;
 KW hypotensive; vasotropic; antiinflammatory; antianginal; anti-HIV;
 KW antiallergic; antiasthmatic; immunosuppressive; antithyroid;
 KW dermatological; antidiabetic; nephrotropic; antitumor; gastrointestinal;
 KW neuroprotective; osteopathic; antiarthritic; uropathic; ophthalmological;
 KW antirheumatic; antiparkinsonian; nootropic; anticonvulsant; hepatotropic;
 KW antiparasitic; haemostatic; cytostatic; antilipemic; antiparasitic;
 KW antihelminthic; antibacterial; virucide; protozoacide; fungicide;
 KW cardiovascular disease; immune system; neurological; growth; development;
 KW cell proliferation; viral; bacterial; fungal; parasitic; protozoan;
 KW helminthic infection; transgenic; gene therapy; enzyme.

OS Homo sapiens.

XX WO2004018641-A2.

XX 04-MAR-2004.

XX 25-AUG-2003; 2003WO-US026635.

XX PR

26-AUG-2002; 2002US-0406172P.
 25-SEP-2002; 2002US-0413910P.
 27-SEP-2002; 2002US-0414296P.
 11-OCT-2002; 2002US-0417821P.

(INCY-) INCYTE CORP.

XX BAUGHN MR, Richardson TW, Marquis JP, Swarnakar A, Tang YT;
 PI Becha SD, Emerling BM, Jin P, Wilson AD, Yue H, Gietzen KU;
 PI Chang H, Yang YG, Lee SY, Khare R, Elliott VS, Hafalia AJA;
 PI Chawla NK, Ramkumar J, Gururajan R, Tribouley CM, Chien D, Tran UK;
 PI Murage J;

XX WPI; 2004-226830/21.
 DR N-PSDB; ADK71922.

XX New human kinases and phosphatases, useful for diagnosing, treating or
 PT preventing atherosclerosis, hypertension, AIDS, allergy, multiple
 PT sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
 PT or hepatitis.

PS Claim 1; SEQ ID NO 40; 347pp; English.

XX The invention relates to a novel isolated polypeptide which is a human
 CC kinase and phosphatase (KPP). The polypeptide of the invention
 CC demonstrates cardiovascular, antiarteriosclerotic, hypotensive,
 CC vasotropic, antiinflammatory, antianginal, anti-HIV, antiallergic,
 CC antidiabetic, immunosuppressive, antithyroid, dermatological,
 CC antiparasitic, nephrotropic, antitumor, gastrointestinal, neuroprotective,
 CC osteopathic, antiarthritic, uropathic, ophthalmological, antirheumatic,
 CC antiparkinsonian, nootropic, anticonvulsant, hepatotropic, antiparasitic,
 CC haemostatic, cytostatic, antilipemic, antiparasitic, antihelminthic,
 CC antibacterial, virucide, protozoacide and fungicide activities. The
 CC kinase and phosphatase (KPP) polynucleotides, polypeptides, agonists and
 CC antagonists may be useful for diagnosing, treating or preventing
 CC disorders such as cardiovascular diseases, immune system disorders,
 CC neurological disorders, disorders affecting growth and development, cell
 CC proliferative disorders and viral, bacterial, fungal, parasitic, cell
 CC protozoan or helminthic infections. Furthermore, the molecules of the
 CC invention may be useful for creating transgenic animals to model human
 CC disease and during gene therapy. The current sequence is that of a human
 CC KPP protein of the invention.

XX Sequence 348 AA;

Query Match 51.0%; Score 639; DB 8; Length 348;
 Best Local Similarity 54.3%; Pred. No. 7.9e-65;
 Matches 126; Conservative 18; Mismatches 16; Indels 72; Gaps 1;

QY 2 NRDKNRYDILPYDSTRVPLGKNDYINASYIRIVNHEEYFYIATQGPLPFIEDFWQM 61
 Db 183 NREKNRYDILPYDSTRVPLGSKNDYINASYIRIVNCGEYFYIATQGPLSTIDFWQM 242
 QY 62 VLENNCNVMIATREIECGVVKCYSWPISLKEPFEHFSVLETFHVTQYFTVRVFOI 121
 Db 243 VLENNCNVMIATREIEGGIKCYHWYPISLKPLKHFVLENYQILQYFIIRMFQV 302
 QY 122 VKSTGSKQCVKHLQFTKPDHGTTPASADFFIKYVRYVRKSHITGPLLHVCSSAGVGTGV 181
 Db 303 VEK-----
 QY 182 FICVDVWFSAIEKNYSFDMINIVTOMRKORCGMIQKEQYCFYIVLVLQ 233
 Db 306 -----SFNMDIVAQMRQSGMWQTKQYHFCYDIVLEVL 342

RESULT 13

ABU70688

ID ABU70688 standard; protein; 766 AA.

XX ABU70688;

XX

DT 10-JUN-2003 (first entry)
DE Human adipocyte Selected Interacting domain, SID, #319.
XX
XX Human; prey; adipocyte; SID; selected interacting domain; anorectic;
KW antidiabetic; protein-protein interaction; diabetes;
KW yeast 2-hybrid assay; metabolic disorder; obesity.
XX
XX Homo sapiens.
XX WO200286122-A2.
XX PN 31-OCT-2002.
XX PD
XX 14-MAR-2002; 2002WO-EP003768.
XX PF
XX 14-MAR-2001; 2001US-0275734P.
XX PR (HYBR-) HYBRIGENICS.
XX PA
XX Legrain P, Daviet L;
XX WPI; 2003-103412/09.
XX DR N-PSDB; ACAS7232.
XX
XX New complex between two interacting proteins in adipocyte cells, useful
PT for identifying selected interacting domains that modulate protein
PT interactions, or for preventing or treating metabolic disorders such as
PT obesity or diabetes.
XX
XX Claim 6; Page 208-209; 382pp; English.
XX
XX The invention relates to a complex between two interacting proteins in
CC adipocyte cells, given in the specification. The proteins are identified
CC by selecting a bait protein from a known adipocyte marker and then
CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by
CC members of an adipocyte cDNA library. The proteins are designated SID
CC (RTM) (selected interacting domains) proteins. Also included are a
CC polynucleotide encoding a polypeptide in the adipocyte cells, a
CC recombinant host cell expressing at least one of the interacting
CC polypeptides of the complex, selecting a modulating compound in adipocyte
CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid
CC sequences given in the specification (including its fragment or variant),
CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences
CC given in the specification (including its fragment or variant), a vector
CC comprising the SID (RTM) polynucleotide, a recombinant host cell
CC comprising the vector, a protein chip comprising the polypeptides and a
CC record comprising all or part of the data, listed in the specification.
CC The complex, polypeptides, polynucleotides and compounds are useful for
CC preventing or treating metabolic disorders such as obesity or diabetes.
CC The polynucleotides are useful as probes or primers. The complex is
CC particularly useful for identifying selected interacting domains (SID
CC (RTM)) for screening drugs that modulate the protein interaction, thus
CC exhibiting the therapeutic effect. The present sequence represents a SID
CC (prey) protein of the invention
XX
XX Sequence 766 AA;
SQ
Query Match 47.3%; Score 592.5; DB 6; Length 766;
Best Local Similarity 47.6%; Pred. No. 6e-59;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;
1 QNRDKNRYDILPYDSTRVPLGKKNKDYINASYIRIVNHEEYFYIATQGLPETIEDFWQ 60
517 ENRRKNRYKILPYDSTRVPLGDEGGYINAFIKIPVCKEEFVYIACQGLPTTVGVDFWQ 576
61 MVLNENNCVMIATREICGVKCYSYWPISL-KEPFEFEHFSVPLETFHTVQFTVRVF 119
577 MIWEQKSTVIAMTQVEGEKIKCQRYWENILGKTTWVSNRLALVRMOQLKGFVVRAM 636
120 QIVKSKTSKSCVQKHLQFTKWPDHGTTPASAFFIKYVRYVRKSHITGPLLHVCAGVGR 179
637 TLEDIQTREVRHISHLNFTAMPDHDTSPQDDLLTFISYMRHRSRSPITHCASAGIRS 696

QY 180 GVFIQVDVWFSAIEKNYSFDMNIVTQMRKQRCMIQTKEQYQCYEIVLEVL 232
DB 697 GTTICIDVVLGLISQLDFDISLVRMRLQRHGMVQTEQYIFCYQVILVVL 749
RESULT 14
AAG67637
ID AAG67637 standard; protein; 1267 AA.
XX
XX AAG67637;
XX 26-NOV-2001 (first entry)
XX DT
XX DE Amino acid sequence of a human protein.
XX KW Human; protein kinase; protein phosphatase; signal transduction.
XX OS Homo sapiens.
XX PN WO200109316-A1.
XX PD 08-FEB-2001.
XX PF 28-JUL-2000; 2000WO-JP005061.
XX 29-JUL-1999; 93JP-00248036.
PR 18-OCT-1999; 93US-0159590P.
PR 11-JAN-2000; 2000JP-00118776.
PR 17-FEB-2000; 2000US-0183322P.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX (HELI-) HELIX RES INST.
XX PA
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
PI Senoo C, Nezu J;
XX WPI; 2001-570286/64.
XX
XX New genes encoding proteins with protein kinase/protein phosphatase
PT activity, useful in the diagnosis and treatment of diseases.
XX
XX Example 4; Page 206-215; 233pp; Japanese.
XX The specification describes human protein kinase/protein phosphatases. It
CC is expected that the protein kinase/protein phosphatase gene participates
CC in signal transduction in cells. The protein kinase/protein phosphatase
CC polypeptides and polynucleotides are useful for developing diagnostics
CC and treatment agents for human and animal diseases. The protein
CC kinase/protein phosphatase polypeptides are useful as target molecules in
CC designing novel drugs. The protein kinase/protein phosphatase
CC polynucleotides are useful as a source of probes and primers, which may
CC be used to isolate homologous sequences. The present sequence represents
CC a human protein, which is used in the course of the invention
XX
XX Sequence 1267 AA;
SQ
Query Match 47.3%; Score 592.5; DB 4; Length 1267;
Best Local Similarity 47.6%; Pred. No. 1.2e-58;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;
1 QNRDKNRYDILPYDSTRVPLGKKNKDYINASYIRIVNHEEYFYIATQGLPETIEDFWQ 60
1018 ENRRKNRYKILPYDSTRVPLGDEGGYINAFIKIPVCKEEFVYIACQGLPTTVGVDFWQ 1077
61 MVLNENNCVMIATREICGVKCYSYWPISL-KEPFEFEHFSVPLETFHTVQFTVRVF 119
1078 MIWEQKSTVIAMTQVEGEKIKCQRYWENILGKTTWVSNRLALVRMOQLKGFVVRAM 1137
120 QIVKSKTSKSCVQKHLQFTKWPDHGTTPASAFFIKYVRYVRKSHITGPLLHVCAGVGR 179

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Db 1138 TLEDIQTRVNRHSHLNTAWPDHDTSPQDDLLTFISYMRHHRSGPIITHCSAGIGRS 1197
Qy 180 GVFCVDVWFSAIEKNYSFDIMNIVTQMRKQRCGMIOQKEQYQFCYEIVLEVL 232
Db 1198 GTLICIDVVLGLISQDLDFDISDLVRCMRLQRHGMVQTEDQYIFCYQVILYVL 1250

RESULT 15
AAG67458
ID AAG67458 standard; protein; 1267 AA.
AC
XX AAG67458;
XX
DT 26-NOV-2001 (first entry)
XX
DE Amino acid sequence of a human polypeptide.
XX
KW Human; protein kinase; protein phosphatase; signal transduction;
KW intracellular signalling pathway.
XX
OS Homo sapiens.
XX
PN W0200109345-A1.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-JP005060.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 18-OCT-1999; 99US-0159590P.
PR 11-JAN-2000; 2000JP-00118776.
PR 17-FEB-2000; 2000US-0183322P.
PR 02-MAY-2000; 2000JP-00183767.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
PI Senoo C, Nezu J;
XX
DR WPI; 2001-564736/63.
XX
XX
XX New genes encoding protein kinase and protein phosphatase, useful for
PT identifying modulators which can be used to treat human or animal
PT disorders associated with the expression or function of these enzymes.
XX
PS Example 4; Page 305-315; 336pp; Japanese.
XX
CC The specification describes human protein kinase/protein phosphatases.
CC The polypeptides are expected to participate in signal transduction in
CC cells. The kinase phosphatases are connected with intracellular
CC signalling pathways. Antisense oligonucleotides and compounds identified
CC by screening (agonists or antagonists) can be used to treat human or
CC animal disorders associated with the expression or function of the
CC protein. In addition, the polypeptides may be used as target molecules
CC for drug development. The present sequence represents a polypeptide, used
CC in the course of the invention
XX
XX Sequence 1267 AA;

Query Match 47.3%; Score 592.5; DB 4; Length 1267;
Best Local Similarity 47.6%; Pred. No. 1.2e-58;
Matches 111; Conservative 41; Mismatches 80; Indels 1; Gaps 1;

Qy 1 QNRDNRYRDLIPYDSTRVPLGKNKDYINASVIRIVNHEEEYFIATQGPLTIEDFWQ 60
Db 1018 ENRRNRYKNILPYDATRVPLGDEGGINASFIKIPVGKEFVIACQGPLTTVGDFWQ 1077
Qy 61 MVLNNCNVIAMITREIECGVIKCYSWPISL-KEPFEHFHSVFLETFHVTQYFTVRVF 119
Db 1078 MIWEQKSTVIAMTQVEGEKIKQRYWPNILGKTTWVSNRLRLALVRMQQLKGFVVRAM 1137
Qy 120 QIVKSKGCKSQVKHLQFTKWDHGTASADFFIKYVRYVRKSHITGPLLHCSAGVGR 179
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Db 1138 TLEDIQTRVNRHSHLNTAWPDHDTSPQDDLLTFISYMRHHRSGPIITHCSAGIGRS 1197
Qy 180 GVFCVDVWFSAIEKNYSFDIMNIVTQMRKQRCGMIOQKEQYQFCYEIVLEVL 232
Db 1198 GTLICIDVVLGLISQDLDFDISDLVRCMRLQRHGMVQTEDQYIFCYQVILYVL 1250
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